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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
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MEDIATNE=87053819; PubMed=2430793;
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13-SEP-2005 (Rel. 48, Last annotation u
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MEDLINE-87058123; PubMed=3097076;
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   MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., As Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McRwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Muhting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G., Anterdield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generzation and initial analysis of more than 15,000 full-length human and manalysis of more than 15,000 full-length human
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MEDLINE=86313660; PubMed=3092219;
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MEDLINE=87080762; Pubmed=3025016; DOI=10.1016/0014-5793(86)81113-9;
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Slightom J.L.;
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'Characterization of single-nucleotide polymorphisms in coding regions
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MEDLINE=97337920; Pubmed=9194591;
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MHMSPALACLVLGLAFVFGEGSTVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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DT 15-JUL-199

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DR REMBL; YIII

DR HSSP; POSS

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               exhibits both overlapping
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GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA
InterPro; IPR00215; Prot_inh_serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meissenheimer L.M., De Lange W.J., Corfield V.A., Moolman-Smook J.
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"Isolation and Characterization of the Vervet Monkey Plasminogen
Activator Inhibitor Type-1 (PAI-1) gene.";

Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the serpin family.

EMBL, AF393201; AAL59139.2; -; mRNA.
                                  and distinct properties with the LDL receptor-related protein.";
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                                                                 Length 402;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 20, Last annotation update)
01-JUN-2003 (TREMBLREL. 20, Last annotation update)
Plasminogen activator inhibitor type-1.
Cercopithecus aethiops (Green monkey) (Grivet)
Bukaryota, Metazoa, Chordata, Cranidata, Vertebrata; Euteleon
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
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Pred. No. 4.5e-158;
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               receptor family,
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PROSITE; PS00284; SERPIN; 1.
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Q8WND4;
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SMART; SM00093; SERPIN; 1
                 (LDL)
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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-!- FUNCTION: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, and protein C. Its rapid interaction with TPA may function as a major control point in the regulation of fibrinolysis.
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plasminogen
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121 FVQRDLKLVQGFMPHFPRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the serpin family.
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Laurasiatheria, Cetartiodactyla, Suina, Suldae,
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15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial
plasminogen activator inhibitor) (PAI)
Name-SERPINEL: Synonyms-PAII, PLANH1;
Sus scrofa (Pig).
Euteleostomi
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97206538; PubMed=9157595;
Bijnens A.P., Knockeart I., Cousin E., Kruithof E.K.O.,
"Expression and characterization of recombinant porcine
activator inhibitor-1.";
Thromb. Haemost. 77:350-356(1997).
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HSSP; PO5121; 9PAI.
SMR; P79315, 26-402.
InterPro; IPR000215; Prot inh serpin.
PANTHER; PTHR11461; Prot Inh eerpin;
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MEDLINE=88329072; PubMed=3262060;
MEDLINE=R329072; PubMed=3262060;
MEDLINE: K., Okada K., Hattori H., Yano M.;
MEAGUTI K., Okada K., Hattori H., Yano M.;
Bovine endothellal Plasminogen activator inhibitor. Purification and heat activation.";
                                                                                                                                                                    1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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Minuro J., Sawdey M., Hatlori M., Loskutoff D.J.;
"CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).";
Nucleic Acids Res. 17:8872-8872[1989].
 PEGMI; PFUULVS; COLPT., PROBLEM; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Glycoprotein; Plasma; Plasminogen activation; Protease inhibitor; Serpin; Signal.
Scrine protease inhibitor; Serpin; Signal.
SIGNAL 1 23 By similarity.
CHAIN 24 402 Plasminogen activator inhibitor-1.
A102 Reactive bond.
A103 Reactive bond.
A104 Reactive bond.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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01-JAN-1990 (Rel. 13, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor) (PAI).
Name-SERPINE1; Synonyms-PAII;
Bos taurus (Bovine).
                                                                       N-linked (GlcNAc. ..) (Potential)
N-linked (GlcNAc. ..) (Potential)
N-linked (GlcNAc. ..) (Potential)
13F60E5F4F8FE405 CRC64;
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                                                                                                                          Score 1790; DB 1; Length 402;
Pred. No. 1.9e-135;
6; Mismatches 29; Indels (
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                                                                                                       45450 MW;
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86.3%;
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Matches 347; Conservative
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402 AA;
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ID PAIL BOVI
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Direct protein sequencing; Glycoprotein; Plasma;
Plasminogen activation; Protease inhibitor; Serine protease inhibitor;
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                                                   Pepper M.S., Belin D., Monteagano R., Orci L., Vassalli J.-D.,
"Transforming growth factor-beta I modulates basic fibroblast growth
factor-induced proteolytic and angiogenic properties of endothelial
cells in vitro.",
J. Cell Biol. 111:743-755 (1990).
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eraction with
                                                                                                                                                              Cell Biol. 11i:743-755(1990).

FUNCTION: This inhibitor acts as "bait" for tissue plasminogen activator, urokinae, and protein C. Its rapid interaction with TPA may function as a major control point in the regulation of
                                                                                                                                                                                                                                                                            -!- SUBUNIT: Interacts with VTN. Binds LRP1B; binding is followed internalization and degradation (By similarity).
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECITY: Vascular endothelial cells may be the prim site of synthesis of plasma PAI.
-!- SIMILARITY: Belongs to the serpin family.
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Reactive bond.
N-linked (GlCNAC. . ) (Potential)
N-linked (GlCNAC. . ) (Potential)
S -> L (in Ref. 2).
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                        TISSUE=Adrenal cortex;
MEDLINE=90338128; PubMed=1696269; DOI=10.1083/jcb.111.2.743;
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9053617333C7D130 CRC64;
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Best Local Similarity 85.3%; Pred. No. 5.9e-135;
Matches 343; Conservative 29; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X16383; CAA34419.1; -; mRNA.
EMBL; X2906; CAA37094.1; -; mRNA.
PIR; S06745; S06745.
SNR; P05121; 9PAI.
SNR; P13909; 25-402.
INCERPO; IPR000215; Prot_inh_serpin.
PANTHER; PTHR11461; Prot_inh_serpin.
Pfan; PP00079; Serpin; 1.
SEQUENCE OF 153-235
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                   GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
                                                                                                                                                                                                                                                                                                                                                                                                         GLASVLAMLQLTTAGETRQQIQEAMRFQIDEKGMAPALRQLYKELMGPWNKDEISTADAI 118
                                                                                                                                                                                        181 DOLTRLVLVNALYFNGOWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD
                                                                                                                                                                                                                                                                                                       Eukaryota, Mētazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                     FVQRDLKLVQCFMPHFPRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
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-!- FUNCTION: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, and protein C. Its rapid interaction with TPA may function as a major control point in the regulation of fibrinolysis.

-!- SUBUNIT: Interacts with VTN. Binds LRP1B; binding is followed by internalization and degradation (By similarity).

-!- SUBCELULIAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89211983; PubMed=3149611; DOI=10.1016/0378-1119(88)90510-0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor) (PAI)
Name-Serpinel, Synonyms-Pail, Planhl;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelenrter T.D.;
"Isolation and characterization of the rat plasminogen activator
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MEDLINE=90130456; PubMed=2298740;
Bruzdzinski C.J., Riordan-Johnson M., Nordby B.C., Suter S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP
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EMBL; M24067; AAA56856.1; -; mRNA.
PIR, A35032; A35032.
HSSP; PO5121; 1LJ5.
SWR; P20961; 27-402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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           FSLETEIDLRRPLENLGMTDMFRPSQADFSSFSDQEFLYVSQALQKVKIEVNESGTLASS 360
                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Plasminogen activator inhibitor: 1 precursor (PAI-1) (Endothelial plasminogen activator inhibitor) (AMI).
Name=SERPINEI; Synonyms=PAI-1, PAII, PLANHI;
Bukstyota; Metazoa; Chordata; Canniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Mustelidae;
MUSEITAXID=9667;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96032362; PubMed=7557448; DOI=10.1016/0378-1119(95)00261-4;
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N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
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                                                                STAVIVSARMAPEEIIMDRPFLEVVRHNPTGTVLFMGQVMEP 402
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45153 MW; DF45E0694DE28401 CRC64;
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85.3%; Pred. No. 6.7e-132;
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PIR; JO4265; JC4265.
HSSP; P05121; 9PAI.
SMR; P50449; 30-400.
InterPro; IPR000215; Prot inh serpin.
PANTHER; PTHR11461; Prot Inh Serpin.
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N-linked
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01-AUG-1991 (Rel. 19, Created)
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R Ensembl; ENSARANCELL THE SET OF THE SET OF
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BS/BGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell; MBDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Alteshul S.F., Zeeberg B., Butcow K.H., Schemer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%; Score 1680; DB 1; Length 402; 80.8%; Pred. No. 1.4e-126;
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Last sequence update)
Last annotation update)
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Best Local Similarity 80.89
Matches 325; Conservative
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Q7TPE9;
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Name=Serpinel;
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360 240 180 240 241 GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300 301 FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360 9 9 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Scherzer R.M., Schmutz J., Wyers R.M., Schmutz J., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY 1 MOMSSALACLILGLVLVSGKGFALPLRESHTAHQATDFGVKVFQQVVQASKDRNVVFSPY GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI FVORDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV DOLTRLVLVNALYFNGOWKTPFFDDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD Gaps STRAIN=B5/EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell; ö Query Match 78.8%; Score 1631; DB 2; Length 402; Best Local Similarity 79.1%; Pred. No. 1.2e-122; Matches 317; Conservative 41; Mismatches 43; Indels Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: Belongs to the serpin family. EMBL; BCO54091; AAHS4091.1; -: mRNA. 402 AA; 45031 MW; 7471F1C3BD83D667 CRC64; 401 401 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVME Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) HSSP; P05121; 1DVM.
SMR; Q7TPE9; 29-401.
MGI; MGI:97608; Serpinel.
GG; GO:0005615; C:extracellular space; TAS.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0045765; P:regulation of angiogenesis; IDA. Ź 402 Prot\_inh\_serpin PROSITE; PS00284; SERPIN; UNKNOWN\_1.

180

240

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QTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWK 286
                                               GHYYDILBLPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
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                                                                                                                       181 DQLTRLVLVNALYFNGQWKTPPPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD
                                                                                                                                                                                                   121 FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
                        GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
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Takafuli V.A., Sharova L.V., Crisman M.V., Howard R.D.;
Takafuli V.A., Sharova L.V., Crisman M.V., Howard R.D.;
Submitted (WAY-2002) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the serpin family.
-- SIMILARITY: BALONGS to the serpin family.
-- HSSP; P05121; 9PAI.
-- SWR; QBM131; 1-280.
-- SWR; QBM131; 1-280.
-- SWR; QBM131; 1-280.
-- SWR; P00004867; F:serine-type endopeptidase inhibitor activity; IEA.
-- InterPro; IPR000215; Prot_inh_serpin.
-- Pfamily PP00079; Serpin; 1.
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Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
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86.4%; Pred. No. 1.2e-92;
.ive 17; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Plasminogen activator inhibitor-1 (Fragment).
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PROSITE; PS00284; SERPIN; 1.
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Q8MI31;
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SEQUENCE
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10-MAY-2005 (Rel. 47, Last annotation update)
Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial
plasminogen activator inhibitor) (PAI).
Name-Serpinel; Synonyms-H1, Pail, Planh!
Nus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria, Buarchontoglires; Glires; Rodentia; Sciurognathi;
Nur maxin-10000.
                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=90158593; PubMed=2406566;
Prendergast G.C., Diamond L.E., Dahl D., Cole M.D.;
"The c-myc-regulated gene mr1 encodes plasminogen activator inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Interacts with VTN. Binds LRP1B; binding is followed by internalization and degradation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interaction with
                                                                                                                                                                                                                                                                                                                                                                                                          Lijnen H.R., van Hoef B., Beelen V., Collen D.;
"Characterization of the murine plasma fibrinolytic system.";
Eur. J. Blochem. 224:863-871(1994).
-!- FUNCTION: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, and protein C. Its rapid interaction with TPA may function as a major control point in the regulation of fibrinolysis.
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N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OSS248:Desc1; NbExp=1; IntAct=EBI-490898, EBI-490889;
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the serpin family.
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                                                                                                                                                                                                                                                                                                                                Mol. Cell. Biol. 10:1265-1269(1990)
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PIR; A34761; A34761.
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45170 MW;
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                                                                                                                                                                                                                                                                                                                                                                        PROTEIN SEQUENCE OF 23-29.
PubMed=7523120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 78.6
Matches 316, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI; MGI:97608; Serpinel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
402
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288
352
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SMR; P22777; 29-402.
IntAct; P22777; -.
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232
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402 AA;
                                                                                                                                                                                     NCBI_TaxID=10090;
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SOURCE TELETER SOURCE BREEF BR

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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Spleen;
                                                                                                                                                                                                                                                          initiative.
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  SOW REAL TO SERVE TO 
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                                                     101 LYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIIN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 DWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTV 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNMTRLPRLLVU,PKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSKELMGPWNKDEISTTDAIFVQRDLKLVQGFWPHFFRLFRTTVKQVDFSDVQRARFIIN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATACOLOGICAL TIGGES S.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the serpin family.
-!- SIMILARITY: Belongs to the serpin family.
HSSP; P05121; 1LJ5.
SMR; O77772; 1-182.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DITHCHPRO; IPR000215; PCCL inh_serpin.
PF00079; Serpin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serpine2-prov protein.
Mameserpina2-prov;
Nanopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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88.5%; Pred. No. 2.9e-61;
ive 13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-ZUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative plasminogen activator inhibitor-1 (Fragment).
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
182 182
182 AA; 20920 MW; B2B6AEB6D92E217F CRC64;
                                                                                                                                386
                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                182 AA.
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                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00093; SERPIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEDD81_XENLA PRELIMINARY;
                                                                                                                                                                                                                                                                                                             O77772_RABIT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LI 182
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NON TER
SEQUENCE
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NEUGREPOLE STREET, WILLIAMS DOI = 10.1073/pnas. 242603899;

A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C., Rabers M.B., Donaldo M.F., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rokanson P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 THRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 EVPLSALTNILSAQLISHWKGNMTRLPR--LLVLPKFSLETEVDLRKPLENLGMTDMFRQ 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESEVERARFIINDWVKTHTKGMISNLLGKGAVD-QLTRLVLVNALYFNGQWKTPFPDSS 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 PLSLEELGSDIGIQVFNQVARTRPHENIVMSPHGISSVLGMLQLGADGRIKKQLMTVMRY
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the serpin family.
BMBL; BC077742; AAH77742.; -; mRNA.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro; IPR000215; Prot_inh_serpin.
                                                                                                                                                                                                                                 Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                          "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                       TISSUE=Spleen;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
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40.7%; Score 842; DB 2; Length 39
Best Local Similarity 45.0%; Pred. No. 4.1e-59;
Matches 170; Conservative 68; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 AA; 43985 MW; 7B0CD19F934AB1EE CRC64;
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Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Dev. Dyn. 225:384-391 (2002).
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datches 159;
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SIGNAL
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RY NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RY MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RY Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Gorden H., Moore T., Max S.I., Wang J., Haiseh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Bas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Lohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

RA Lilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Hatesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Monice Chur Schein J.E., Jones S.J.M., Marra M.A.;

Rederzetion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                      FQADFISLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEBIIMDRPFLFV 384
                                                                                                     STPLSAIIPHISTKTLQSW----MTMSPKRVQLILPKFSVEAEADLKEPLRNLGITEMFDV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                       GOOD MOUSE STANDARD; PRT; 397 AA.

007215; Q92177;
01-072177;
01-07218 (Rel. 30, Created)
01-07218 (Rel. 31, Last sequence update)
01-07218 (Rel. 31, Last annotation update)
01-07218 (Rel. 47, Last annotation (Protease nexin I) (PN-1) (Serine protease-inhibitor-4).
02-07218 (Mouse)
03-07218 (Mouse)
0
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EMBO J. 12:1871-1898(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLUTAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Most abundant in seminal vesicles.
-!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belin D.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muroidea; Muridae; Murinae; Mus.
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378 IRHNPTGAVLFTGQINKP 395
                                                                                                                                                                                                              VRHNPTGTVLFMGQVMEP 402
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94 MAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFWPHFFRLFRSTVKQVDFSEVE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 LINILSAQLISHWKGNMTRLPRLLVLPKFSLBTEVDLRKPLENLGMTDMFRQFQADFTSL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 SDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEELIMDRPFLFVVRHNPTGT 392
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
16-days embryo head colNA, RIKEN full-length enriched library,
clone:Cl30010H12 product:serine (or cysteine) proteinase inhibitor,
clade E (nexin, plasminogen activator inhibitor type 1), member 2,
full insert sequence (12 days embryo spinal ganglion cDNA, RIKEN full-
length enriched library, clone:Dl30035K01 product:serine (or cysteine)
proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor
type 1), member 2, full insert sequence) (Adult male corpora
quadrigemina cDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                           PROSITE; PS00284; SERPIN; 1. Developmental protein; Heparin-binding; Developmental protein; Differentiation; Glycoprotein; Heparin-binding; Neurogenesis; Protease inhibitor; Serine protease inhibitor; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 LASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGFKIDDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 RARFIINDWVKTHTKGMISNLLGKGAVD-QLTRLVLVNALYFNGQWKTPFPDSSTHRRLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 HKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
Glia derived nexin.
Reactive bond (By similarity).
N-linked (GlcNAc. .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.5%; Score 796.5; DB 1; Length 397; 43.0%; Pred, No. 1.9e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 I -> V (in Ref. 2).
44207 MW; B8EBAE3CA899D4A5 CRC64;
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                                                                                                 HSSP, PO5121; 1DB2.
Ensembl; ENSMUSGO00026249; Mus musculus.
MG1; MG1: 101780; Serpine2.
GO; GO:0005615; C:extracellular space; TAS.
EMBL; X70296; CAA49777.1; -; mRNA.
EMBL; BCO10675; AAH10675.1; -; mRNA.
EMBL; X70946; CAA50285.1; -; Genomic_DNA.
PIR: 148717; 148717.
                                                                                                                                                                                               InterPro; IPR000215; Prot inh serpin. PANTHER; PTHR11461; Prot_Inh_serpin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Q543RS;
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                                                                                                                                                                                                                                                 Pfam; PF00079; Serpin; 1.
                                                                                                                                                                                                                                                                                 SMART; SM00093; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 VLFMGQVMEP 402
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ILFLGQVNKP 397
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397
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159
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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Azakawa T., Izawa M., Nibhi K., Kiyoswa H., Kodoo S., Yamanaka I., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rudel P., Lewis S., Matsudo H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pecole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sator K., Sato K., Sator K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., T., Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J;
TISSUE=Head, Spinal ganglion, and Corpora quadrigemina;
MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
   one:B230326M24 product: serine (or cysteine) proteinase inhibitor, ade E (nexin, plasminogen activator inhibitor type 1), member 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE-Corpora quadrigemina, Head, and Spinal ganglion;
MEDLINE-21085660; PubMed-11217851; DOI-10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meth. Enzymol. 303:19-44(1999).
                                                            insert sequence).
                                                                                                                                                                                                       Muridae; Murinae; Mus
                                                                                                                     Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J;
                                                                                    Name=Serpine2;
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C STRAIN-CSTBL/GS.

G STRAIN-CSTBL/GS.

G TISSUB-CSTBL/GS.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Aukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hundagaki T., Hara A., Hashizume W., Hayashida K., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hanagaki T., Hara A., Hashizume W., Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Makatoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Murata M., Nakamura M., Nahi K., Nomura K., Numazaki R., Ohno M., Ohaton N., Okazaki Y., Saito R., Saito R., Sakai K., Sakazume N., Sano H., Santo R., Saito R., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Toka T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DbbJ databases.

L. SIMILARITY: Belongs to the serpin family.

EMBL; AKO47856; BAC33161; -; mRNA.

MGI; MGI:101780; Serpine2.

R. Goloosels; C:extracellular space; TAS. 94 MAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVE 153 148 SASESINFWVKNETRGMIDNLLSPNLIDGALTRLVLVMAVYFKGLWKSRFQPESTKKRTF 207 208 VAGDGKSYQVPMLAQLSVFRSGSTRTPNGLWYNFIELPYHGESISMLIALPTESSTPLSA 267 CTRAIN-C57BL/6J;

CTRAIN-C57BL/6J;

X MEDLINE-20530913; PubMed=1107661; DOI=10.1101/gr.15260;

MEDLINE-20530913; PubMed=1107661; DOI=10.1101/gr.15260;

A Shibata K., Itoh M., Aizawa K., Nagaoka S., SaBaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watehiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y., Ranaka T., Ranaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ranaka T., Matsuura S., Kawai J., Sokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; TISSUE=Corpora quadrigemina, Head, and Spinal ganglion;
MEDILINE=20499374; PubMed=11042119; DOI=10.1101/dr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000). 'Analysis of the mouse transcriptome based on functional annotation of 34 LASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGFKIDDKG 213 HKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSA 154 RARFIINDWVKTHTKGMISNLLGKGAVD-QLTRLVLVNALYFNGQWKTPFPDSSTHRRLF Length 397; 397 AA; 44207 MW; B8EBAE3CA899D4AS CRC64; 38.5%; Score 796.5; DB 2; 74; Mismatches 134; Pred. No. 1.9e-55; 60,770 full-length cDNAs."; Nature 420:563-573(2002). 43.0%; Best Local Siminary, Matches 159; Conservative NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE STRAIN=C57BL/6J; SEQUENCE Query Match Serpin. g g g ò ò ð 8 유

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 133-153 AND 347-397, AND FUNCTION.
MEDLINE=90248459; PubMed=2337608;
MICK H., Hofsteenge J., Shaw E., Rovelli G., Monard D.;
Functional sites of glia-derived nextn (GDN): Importance of the site reacting with the protease "".
Blochemistry 29:441-421(1990).
I- FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting trypsin, and urokinase.
I- SUBCELLULAR LOCATION: Extracellular.
--- SUBCELLULAR Belongs to the serpin family.
                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
MEDLINE=88107544; PubMed=3427015;
Sommer J., Gloor S.M., Rovelli G.F., Hofsteenge J., Nick H., Meier R.,
Monard D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGFKIDDKG
                  01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Glia derived nexin precursor (GDN) (Protease nexin I) (PN-1).
Name-Serpine2; Synonyms-Pi7, Pn1;
Rattus norvegicus (Rat).
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P05121, 1DB2.
RGD; 3748; Serpine2.
GG; GG: 0004867; P: serine-type endopeptidase inhibitor activity; TAS.
InterPro; IPR000215; Prot_inh_serpin.
PANTHER; PTHR11461; Prot_inh_serpin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "CDNA sequence coding for a rat glia-derived nexin and its homology members of the serpin superfamily."; Biochemistry 26:6407-6410(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE OF 82-96; 165-178 AND 317-333, AND HEPARIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ffam; PF00079; berg..., -...
SMART; SM0093; SERPIN; 1.
PROSITE; FS00284; SERPIN; 1.
Developmental protein; Differentiation; Direct protein sequencing; Glycoprotein; Heparin-binding; Neurogenesis; Protease inhibitor; Serpin; Signal.
Scrine protease inhibitor; Serpin; Signal.
SIGNAL.
20 397 Glia derived nexin.
CHAIN 20 397 Glia derived nexin.
SITE 364 365 Reactive bond (Potential).
SITE 159 N-linked (GlCNAC. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rovelli G., Stone S.R., Guidolin A., Sommer J., Monard D.; "Characterization of the heparin-binding site of glia-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.7%; Pred. No. ...
Live 72; Mismatches 137;
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42.7%; Pred. No. 4.8e-55;
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PIR; B27496; B27496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 31:3542-3549(1992).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 MAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFWPHFFRLFRSTVKQVDFSEVE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDOEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEELIMDRPFLFVVRHNPTGT 392
                                                                                                                   SDGEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGT 392
                                                                                                                                               LINILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSL 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 LGSNTGIQVFNQIIKSRPHENVVVSPHGIASILGMLQLGADGKTKKQLSTVMRYNVN--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 SASESINFWVKNETRGMIDNLLSPNLIDGALTRLVLVNAVYFKGLWKSRFQPESTKKRTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 VAGDGKSYQVPMLAQLSVPRSGSTRTPNGLWYNFIELPYHGESISMLIALPTESSTPLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E., Mollenhauer J., Wiemann S., Schick M., Korn B.; "Cloning of mouse full open reading frames in Gateway(R) system entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 HKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus muscúlus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Mus.
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38.5%; Score 796.5; DB 2; Length
Best Local Similarity 43.0%; Pred. No. 1.9e-55;
Matches 159; Conservative 74; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector (pDONR201).";
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CT010311; CAJ18519.1; -; mRNA.
SEQUENCE 397 AA; 44193 MW; F7F5413CBEE36863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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13-SEP-2005 (TrEMBLrel. 31, Le
13-SEP-2005 (TrEMBLrel. 31, La
Serpine2 protein.
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Q4FJU1;
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ILFLGQVNKP 397
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RESULT 15

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Search completed: December 13, 2005, 09:08:39 Job time : 235 secs

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1 MOMSPALITCLVLGLALVFGE......FVVRHNPIGTVLFMGQVMEP 402
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2004s:*
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw31587 Human pla	_	_	-		5 Human		Human	Human	Human	Human		Human	Adj75605 Marker ge	Adl35812 Human pla	Ado05046 Human pla	-	Adp23374 PRO polyp	Adq39257 Human myo	Adq39256 Human myo		Aea81039 Human pla	-	Aar07986 Plasminog
SUMMARIES	ΙD	AAW31587	AAU04913	AAB90794	ABP65137	AAE14271	ABP68605	AAE37131	ABR82199	ABR63123	ADF28929	ADF28771	ABW02690	ADN95544	ADJ75605	ADL35812	ADO05046	ABM80915	ADP23374	ADQ39257	ADQ39256	ADV70216	AEA81039	AEB29725	AAR07986
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	Score	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2071	2067
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/label= Pl /note= "preferred substitution site to provide elastase inhibitor mutant" Misc-difference 377

/note= "preferred substitution site for protein

/note= "preferred substitution site to provide elastase inhibitor mutant"

/label= P4

Misc-difference 366

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				386	۸ د	ABR63124	Abr63124 Human pla	
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	٠	958		379	S.	AAU97221	Aau97221 Wild-type	
		957		379	~	AAW26718	Aswze/is Fiasminog	
		957		2 / L	4 ~	AA004928 AAB08411	Aar08411 Modified	
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		955		379	4	AAU04925	Aau04925 Human Pla	
		954		379	7	AAW26714	Aaw26714 Plasminog	
		954		379	4	AAU04922	Aau04922 Human Pla	
		952		379	~	AAW26710	FIABRI	
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ş y	AAW31587	587;						
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TO X	14-AE	-APR-1998	(IIIBC	Bc entry)	2			
E B	Humar	Human plasminogen	nogen	activator	ator	inhibitor type 1.		
××		)					•	
Σ.	Plasn	ninogen	activ	rator in	dida	Plasminogen activator inhibitor type 1; PAI-1; human;	human; elastase innibitor; cell proliferation:	
MX.	VICE Onsp.	nectin;	11.	1; cell accaciment	1 0	٠.	acute lung inflammation;	
2 2	מלקווה פלקן	alpha 1-antitronsin	LTVDB	in defi	icie	- 10	; atopic dermatitis;	
ž	Danci	reatitie	i; per	iodont	al d	Ξ	atherosclerosis;	
KW	reste	nosis;	neoir	tima;	fibr	nd healing;	tumour; metastasis;	
¥.	psoriasi	iasis; t	hrom	thrombosis; a	angi	angiogenesis; therapy.		
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E	Key		1	ocation	n/9	Location/Qualifiers		
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(first entry)

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Human Plasminogen activator inhibitor-1, PAI-1.
                                  26-SEP-2001
            AAU04913;
                                                                                                                                                                                                                                                                                      Region
  ö
                                                                                                                                                                                                                                                This polypeptide sequence comprises wild-type human plasminogen activator inhibitor type (PAI-1). Novel mutants (see AAW6710-25) of the PAI-1 mature protein are claimed that inhibit elastase or other elastase-like proteases, or are inhibitors of vitronectin-dependent cell migration. The mutants are obtained by site-directed mutagenesis of the PAI-1 DNA sequence (see AAT97303) and expression in host cells, and have a range of therapeutic uses. Preferred mutants have amino acid substitutions in the reactive centre loop region (especially at position 343 and/or 346 of the muture protein), and may have additional stabilising amino acid substitutions at 1-4 of residues 150, 154, 319 and 354, and 1-5 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTBFTTPD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
                                                                                                                                                                                   Plasminogen activator-inhibitor type I mutant inhibits elastase - or has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MQMSPALTCLVJGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MOMSPALICLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2071; DB 2; Length 402; 100.0%; Pred. No. 4.4e-190; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                              Claim 3; Fig 4A; 144pp; English.
                                                                                                          (AMNA-) AMERICAN NAT RED CROSS
  substitution"
                                                                                     96US-0015299P
                                                                97WO-US006071
                                                                                                                                 SP;
                                                                                                                                Stefansson
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 402; Conservative
                                                                                                                                                     WPI; 1997-526399/48
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                N-PSDB; AAT97303
                                                                                                                                                                                                                                                                                                                                                                                   Seguence 402 AA;
                     WO9739028-A1
                                                                11 -APR-1997;
                                                                                      12-APR-1996;
                                                                                                                                Lawrence DA,
                                           23-0CT-1997
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The sequence represents human plasminogen activator inhibitor-1, PAI-1, a serine proteinase inhibitor or serpin. The protein is used to demonstrate the method of the invention which comprises detecting a functionally active form of an enzyme in a biological sample by contacting an enzyme inhibitor immobilised on a solid substrate with the biological sample and measuring the binding of the enzyme inhibitor to the active form of the enzyme inhibitor specifically forms a covalent bond or binds with a dissociation constant of 1 x 10-9W forms a covalent bond or binds with a dissociation constant of 1 x 10-9W forms a covalent bond or binds with a dissociation of a functionally active form of an enzyme in a biological sample. Human PAI-1 can be used to detect a number of enzymes including tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil elastese, pancreatic elastese, trypsin, cathepsin G and prostate specific antigen and as such can be used in methods to diagnose diseases such as cystic fibrosis, acute respiratory distress syndrome (ARDS), HIV infection, TWF-mediated inflammation, prostate and benign prostatic hypertrophy
Human, Plasminogen activator inhibitor-1, PAI-1; serpin, immobilised enzyme, cystic fibrosis, acute respiratory distress syndrome, ARDS; HIV infection, Human immunodeficiency virus; prostate cancer; TNF-mediated inflammation; benign prostatic hypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilized on a solid substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Mature PAI 1 #2
//note= "Both mature forms are detectable in vivo"
357. 374
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                                                                                                                                                                                                                                                                                                                                                                                                        l. .21
/label= Signal_peptide
/note= "Alternative signal peptide"
                                                                                                                                                                                                                                                                                                 1. .23
/label= Signal_peptide
/note= "Alternative signal peptide'
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/label= Reactive_centre_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mature_PAI-1 #1
                                                                                                                                                                                                                                                       Location/Qualifiers
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Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell
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                                                                                                                               GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
                                                                                                                                                                                     121 FVORDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
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                                                                          1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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                      Score 2071; DB 4;
Pred. No. 4.4e-190;
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                        100.0%;
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08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
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                                                    Conservative
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                                     Local Similarity
nes 402; Conserv
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Sequence 402
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                                                                                  DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD
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                                                                                                                        FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
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               MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and hypertension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
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Nakamura Y, Sugano S;
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useful in diagnosis and
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N-PSDB; AAH02917.
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                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                        19-FEB-1998;
                                          Unidentified
                                                                    US6303338-B1
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                                                            The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type indicated in a disease or conditions, and identifying a gene that is differentially regulated in the two pecialised cell types under experimental conditions. ABV73816 and ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating adlesses in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological release to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, precelapmia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
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 under different conditions and identifying a differentially
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                                                                                                                                                                                                                                                                                                                                         Length 402;
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100.0%; Pred. No. 4.4e-190;
iive 0; Mismatches 0;
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                                       Claim 35; Page 338; 538pp; English
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(first entry)
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                                                                                                                                                                                                                                                                                                              Sequence 402 AA;
              regulated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to nucleic acids encoding pancreas-derived plasminogen activator inhibitor (PARI) protein. Plasminogen activator inhibitor (PARI) protein. Plasminogen activator inhibitor (FARI) in and 2 are involved in many physiological and pathological processes, including normal pregnancy, preeclampsia, intrauterine growth retardation, wound healing, tumour cell invasion and metastasis, inflammation and arthritis, inflammatory bowel disease, appendicitis, complications from systemic lupus erythematosus, ovulation and prostatic involution and osteonecrosis. PARAI DNA is used to treat physiological and pathological conditions including breast cancer and to present amino acid sequence is a PAI protein. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polynucleotides encoding the pancreas-derived plasminogen estivator inhibitor protein are useful to treat physiological and pathological conditions including breast cancer, and to detect pathological disorders.
systemic lupus erythematosus; ovulation; cytostatic; gene therapy;
prostatic involution; osteonecrosis; breast cancer; pregnancy.
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360

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The invention relates to an isolated polymucleotide (I) comprising: (a)

any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)

complements of (a); (c) sequences consisting of at least 20 contiguous

residues of (a); (d) sequences that hybridize to (a), under moderately

stringent conditions; (e) sequences having at least 75 or 90% identity

to (a); or (f) degenerate variants of (a) Polypeptides (ABP68596-

CC ABRE6837) encoded by (I) and oligonucleotide can be used to defect cancer

in a patient and compositions comprising polypeptides, polymucleotides,

antibodies, fusion proteins, T cell populations and antigen presenting

cells expressing the polypeptide are useful in treating pancreatic cancer

and stimulating an immune response. The polymucleotides can be used as

probes or primers for nucleic acid hybridisation, in the design and

preparation of ribozyme molecules for inhibiting expression of the tumour

prophypeptides and proteins in the tumour cells, in vaccines and for gene

therapy. Note: The sequence data for this patent did not form part of the

primed specification, but was obtained in electronic format directly

from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiang Y;
                                                                                                                                                            cancer; gene therapy; vaccine; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            new isolated polynucleotide and pancreatic tumor polypeptides, diagnosing, preventing and/or treating cancer, particularly pancancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persing DH, Hepler WT,
                                                                                                                             Human pancreatic cancer expressed protein SEQ ID NO 154.
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               ABP68605 standard; protein; 402
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99-FFB-2001; 2001US-0267568P.

21-MAR-2001; 2001US-0287112P.

28-APR-2001; 2001US-0291631P.

16-MAY-2001; 2001US-0291631P.

12-UUL-2001; 2001US-0305484P.

20-AUG-2001; 2001US-030599P.
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27-NOV-2001; 2001US-0333626P
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                                                                                                                                                                                                                         Homo sapiens.
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ABP68605
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                                                                                                                                                                  The invention relates to a method for treating or preventing arthritis e.g. osteoarthritis, rheumatoid arthritis in mammals, by administering inhibitors of plasmin, plasminogen, urokinase-type plasminogen activator (uPA), plasminogen-activator inhibitor type 1 (PAI-1) and urokinase-type plasminogen activator receptor (uPAR). The method is useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteoarthritis, rheumatoid arthritis, plasmin, plasminogen, human, urokinase-type plasminogen activator; uPA; degenerative joint disease; spondyloarthropathy; antisense-therapy; antibody therapy; osteopathic; urokinase-type plasminogen activator receptor; psoriatic arthritis; plasminogen-activator inhibitor type 1; PAI-1; uPAR.
                                                              GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK
          PSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQBPLHVAQALQKVKIEVNESGTVASS
                                              FVORDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
                                                                                                  DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating or preventing arthritis e.g. osteoarthritis, rheumatoid arthritis in mammals, by administering inhibitors of plasmin, plasminogen, urokinase-type plasminogen activator or plasminogen activator inhibitor type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human plasminogen-activator inhibitor type 1 (PAI-1) protein.
                                                                                                                                                                                                                                                         STAVIVSARMAPEELIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
                                                                                                                                                                                                                                                                        Disclosure, Page 82-83; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                      AAE37131 standard; protein; 402 AA
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10-JUL-2001; 2001US-0304490P.
13-JUL-2001; 2001US-0305182P.
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Best Local Similarity 100. Matches 402; Conservative

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or preventing arthritis caused by degenerative joint disease, preferably rheumatoid arthritis, psoriatic arthritis, infectious arthritis, juvenile rheumatoid arthritis, osteoarthritis and spondyloarthropathise in a mammal, especially a human. It is also useful for identifying agents for treating or preventing arthritis in a mammal and it is also useful in antisense-therapy and antibody therapy. The present sequence is human PAI
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                                                                                                   1; DB 6;
4.4e-190;
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                                                                                                 100.0%; Score 2071;
100.0%; Pred. No. 4.4
tive 0; Mismatches
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/label= signal
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| Jabel= PAI-1
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                                                                               Sequence 402
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                                                                                                   Query Match
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The present invention describes a mutant proteinase inhibitor (I) accomprising a wild-type proteinase inhibitor amino acid sequence with at least I mutation in at least I epitope of the amino acid sequence, where the mutation alters the binding of the mutant proteinase inhibitor to an anti-proteinase inhibitor to the anti-proteinase inhibitor to the anti-proteinase inhibitor of the anti-proteinase inhibitor of a screening at least one compound that affects the activity of a proteinase inhibitor. (I) is also useful for screening at least one compound that affects the inhibitor. The present sequence represents human plasminogen activator inhibitor. The present sequence represents human plasminogen activator inhibitor I (PAI-I), which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                        nover mutant proteinase inhibitor comprising a mutation in an epitope amino acid sequence of wild-type proteinase inhibitor, useful for screening compounds that affect inhibitory activity of the proteinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVASVLAMLOLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTBFTTPD
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; Pred. No. 4.4e-190;
0; Mismatches 0;
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Crandall DL;
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                                                                                                                                                                                                                                                                      Claim 8; Fig 1; 46pp; English
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  Gorlatova N,
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Best Local Similarity 100.0
Matches 402, Conservative
                                                  WPI; 2003-569214/53.
N-PSDB; ACF06144.
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  Lawrence DA,
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FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360
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100.0%; Pred. No. 4.4e-190;
iive 0; Mismatches 0;
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/label= Signal_peptide
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                                                                                                                                                                                                    ADF28929 standard; protein; 402
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                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                      RESULT 10
                                                                                                                                                                                     ADF28929
ID ADF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of human plasminogen activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce activator inhibitors. Such PAI-1 inhibitors can be used to produce inhibitors. Such PAI-1 inhibitors can be used to treat a warm-blooded vertebrate animal having a medical condition, e.g. alopecia, undesired weight loss, Alzheimer's disease, systemic amyloidosis, myclifosis, glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne, atherosclerosis, ageing, or a wound (claimed). A method of testing a candidate composition for PAI-1 inhibition activity comprises.

Candidate composition to a transgenic animal having a PAI-1 gene incorporated into its genome, and observing an ameliorating change in the improvement of a vascular thrombotic disorder, asthma, chronic improvement of a vascular thrombotic disorder, asthma, chronic cobstructive pulmonary disease, alopecia, undesired weight loss such as anorexia, Alzheimer's disease, systemic amyloid deposition, bytance.
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hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Treating a warm-blooded vertebrate animal having a medical condition, e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or glomerulosclerosis, comprises administering a plasminogen activator inhibitor-1 inhibitor.
           antidepressant; nephrotropic; vulnerary;
dermatological; antiarteriosclerotic; hepatotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 62-64; 91pp; English.
                                                                                                                                                                                                                                                                                                    Eren M;
                                                                                                                                                                                                             19-FEB-2002; 2002US-0358061P.
                                                                                                                                                                       19-FEB-2003; 2003WO-US005008
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                                                                                                                                                                                                                                               UNIV VANDERBILT.
DECLERCK P J.
                                                                                                                                                                                                                                                                                                                                        WPI; 2003-721694/68.
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             neuroprotective;
antiseborrhoeic;
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                                                                                                    WO2003071267-A1.
                                                                  Homo sapiens
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precursor. This is an example of a therapeutic protein that can be encoded by an adeno-associated virus (AAV) vector of the invention. Such vectors comprise a promoter operably positioned upstream of a nucleic caid encoding a biologically-active therapeutic mammalian serpin or cytokine polypeptide, and operably positioned an enhancer sequence cytokine polypeptide, and operably also include an enhancer sequence cytokine polypeptide, and operably also include an enhancer sequence comprising the vector, and a mammalian cell, spleen, liver, heart, lung, islet, hepatocyte, pancreas, kidney, muscle, spleen, liver, heart, lung, or brain cell, one the vector are claimed. A claimed composition comprising the vector are claimed. A claimed composition comprises the vector, the recombinant AAV virion, AAV viral particles, or the mammalian cell, and is used in cancer, diabetes, autoimmune disease, comprises the vector disease therapy. The composition is also used in claimed methods for preventing type I diabetes, and for reducing the control of disease progression of type I diabetes, in a human.
New adeno-associated viral vector, useful in preparing a composition for treating or preventing e.g., cancer, diabetes, or autoimmune, pancreatic or liver disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; plasminogen activator inhibitor 1; gene therapy; cytostatic;
antidiabetic; immunosuppressive; hepatotropic; adeno-associated virus.
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/label= Plasminogen activator inhibitor 1
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plasminogen-activator inhibitor-1; PAI-1; breast cancer; tumour;
cancer therapy; human.
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N-PSDB; ADF28770.
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as low risk (LR) if the upA level is below a cut-off value of between the CC 55 th . and 75 th percentile of normalized or analogous upA in a cc randomized population of breast cancer patients, and if the PAL: level is lower than a cut-off value between the G1 st and 81 st percentile in the same population, or as high risk (HR) if the levels of upA and PAI: cc are above these cut-off values. The treatment of LR (or HR) patients is then selected as one that results in the highest expected benefit in a comparable population of LR (or HR) patients. The method is used: for selection of the most effective therapy, including one designed to prevent relapse; and to predict expected benefit, overall or disease-free cutvival in patients with cancer, particularly of the breast but also lenkemia and plasmacytoma. The method can also be used: to predict the CS curvival in patients with cancer, particularly of the breast but also lenkemia and plasmacytoma. The method can also be used: to predict the CS concernation to relapse of cancer, especially where CC benefit of preventative treatment for relapse of cancer, especially where CC benefit of preventative treatment for relapse of cancer, especially where CC deciding whether or not to administer an aggressive or non-aggressive regime; and for candinistered; in this case HR patients are those who are estrogen- and/or progesterone- receptor positive). The present sequence represents a human can an or the contract of the contrac
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                                                                                                                   New catalytic nucleic acid that hybridizes to and specifically cleaves mRNA encoding a Plasminogen Activator Inhibitor-1, useful in preparing composition for treating e.g., cardiovascular or fibrotic disease.
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lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
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                                                                                                                                                                                                                                                           DB 7; Length 402;
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100.0%; Pred. No. 4.4e-190;
ive 0; Mismatches 0;
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                                                                                                                                                         Disclosure; SEQ ID NO 6; Opp; English
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                   23-APR-2002; 2002US-00128706.
                                     23-APR-2002; 2002US-00128706
                                                                                         WPI; 2003-852809/79.
N-PSDB; AAD64644, AAD64654.
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                                                                                                                                                                                                                                                                      Similarity
                                                       (ITES/) ITESCU S.
                                                                                                                                                                                                                                          Sequence 402 AA;
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  23-OCT-2003
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composition or differentiation or blood endocthelial cells with a composition comprises contacting endothelial cells with a composition comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoddema comprises identifying a human subject with lymphoddema comprises or correlates with lymphoddema in human subjects, and with a mutation in at corposition comprising a LEC protein, where the mutation correlates with lymphoddema in human subjects, and with the proviso that composition comprising a luc protein, where the mutation corposition comprising a luc growth agent selected from WeGF-C verge-D polypeptides and polymucleotides. The invention may be useful for the development of composition with an antianglogenic, cytostatic, cytostatic, conductedial cells or lymphatic endothelial cells, in treating heredy. The method is useful in modulating the growth or differentiation of blood conducted in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cells or lymphatic vessel endothelial cell growth or differentiation. The cell or lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a cibc gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases involving the lymphatic vessels, such as various inflammatory diseases involving the lymphatic vessels, such as various inflammatory diseases involving the lymphatic vessels, such as cytoses doctor which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic
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lymphatic growth agent; VEGF-C; VEGF-D; antianglogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; human.
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100.0%; Pred. No. 4.4e-190;
ive 0; Mismatches 0;
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nes 402; Conservative
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(LICN ) LICENTIA LTD
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WPI; 2004-239116/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy expression level of the marker gene comprises; and a bealthy constitute pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial compound, cobstructive pulmonary disease; (7) a marker gene or an antisense nucleic acid corresponding to a portion of
                                       FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360
                                                                                           DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD 240
                        GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
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                                                                                                                                                                                                                                                                                                                           bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory;
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                                                                                                                                            Marker gene related amino acid sequence SEQ ID NO:857.
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2003JP-00077212.
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the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene, and (1) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent charapt for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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Pred. No. 4.4e-1
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                Sequence 402 AA;
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GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
                                                                                                                                                                                                                              Producing an antibody that specifically binds to pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptide comprises introducing the polypeptide to the animal, and recovering the antibody.
                                                                                                                                                                                                                                                                                                                            The present invention provides pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptides and their encoding polymucleotides. The invention is useful for producing an antibody that specifically binds to pancreas-derived plasminogen activator inhibitor (PAPAI) polypeptide. The present sequence is human plasminogen activator inhibitor (PAPAI) protein.
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100.0%; Pred. No. 4.4e-190;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                 Disclosure, SEQ ID NO 3; 51pp; English
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          96US-0024056P.
97US-00934011.
98US-00026408.
2001US-00902684.
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                                                                                                                                                                       Ruben SM,
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                                                                                                                                                                                                     WPI; 2004-356204/33.
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                                                                                        NI J.
GENTZ R I
RUBEN S N
SHI Y E.
                                                                                                                                                                       Gentz RL,
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          16-AUG-1996;
15-AUG-1997;
19-PEB-1998;
                                                            12-JUL-2001;
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                                                                                                                                    The invention relates to a novel method for identifying a compound that modulates angiogenesis which comprises contacting the compound with a nucleic acid, or a polypeptide encoded by a nucleic acid, that hybridises under stringent conditions to a second nucleic acid and determining the functional effect of the compound upon the nucleic acid or polypeptide. The method of the invention has cytostatic applications and may be useful for identifying a compound that modulates angiogenesis for treating cancer or for use during gene therapy procedures. The current sequence is that of an angiogenesis-related human protein of the invention.
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                            Identifying a compound that modulates angiogenesis for treating e.g., cancer comprises contacting the compound with a nucleic acid or polypeptide and determining the functional effect of the compound upon the nucleic acid or polypeptide.
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                                                                                                                                                                                                                                                                                                                                   / Match 100.0%; Score 2071; DB 8; Local Similarity 100.0%; Pred. No. 4.4e-190. nes 402; Conservative 0; Mismatches 0;
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                                                                                                            Claim 19; SEQ ID NO 420; 245pp; English
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 ADL35811
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Gaps

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Length Indele 180 240 240

180

120

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300

360

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polypeptide PRO2604, SEQ:2362

PXBXBXBXBXBXBXBX

GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide polypeptides to relates to nucleic acid and polypeptide polypeptides expression vectors and host cells comprising a TAT nucleic acid, an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; molecule which binds to a TAT polypeptide; molecule or organic molecule which binds to a TAT polypeptide; mucleic acids, antibodies, and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides mucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosis of cancer in mammals. TAT polypeptides associated with increased TAT expression, particularly cancers such as breast cancer, cancer, pancreatic cancer, cancer, cancer, bladder cancer, pancreatic cancer, cervical cancer, pancreatic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New tumor-associated antigenic target polypeptides and nucleic acids,
tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; lovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukemin; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; SEQ ID NO 2362; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2002; 2002US-0414971P.
                                                                                                                                 gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-347921/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ACN38690
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                                                                                                                                                                                  Homo sapiens.
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ö GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120 FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV 180 FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV 180 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD 240 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMAAQTNKFNYTEFTTPD 240 9 1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY 1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY Gaps ; 0 Length 402; Indele 100.0%; Score 2071; DB 8; 100.0%; Pred. No. 4.4e-190; ; 0 Mismatches ó Conservative Local Similarity nes 402; Conserva 181 Query Match 61 61 121 121 181 Matches 용 ઠે g ò g 8

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The invention relates to a novel isolated nucleic acid and the PRO
polypeptide encoded by it. A protein of the invention has
antiinflammatory, antiarthritic, antirhemmatic, immunosuppressive,
cateopathic, antidabetic, dermatological, antipsoriatic, antiallergic,
antiasthmatic, hepatotropic, and respiratory activity. A polymucleotide
of the invention may have a use in gene therapy. The PRO polypeptide, its
agonist, antagonist, or antibody that specifically binds to the
polypeptide is useful for treating an immune related disorder such as
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
idiopathic inflammatory myopathy, Sjogran's syndrome, systemic
vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
disease, a demyelinating disease of the central or peripheral nervous
system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
disease, infectious or autoimmune chronic active hepatitis, primary
bilary cirrhosis, granulomatous hepatitis, selecoathy, Whipple's
inflammatory bowel disease, gluten-senatitive enteropathy, Whipple's
clisease, an autoimmune or immune-mediated skin disease, a bullous skin
                                               360
      241 GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
                                                                                301 PSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                         PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood WI;
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                                                                                                                             STAVIVSARMAPEELIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
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                                                                                                                                                  STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGOVMEP
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                                                                                                                                                                                                                                                                   ADP23374 standard; protein; 402
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                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark H, Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-419628/39.
N-PSDB; ADP23373.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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       disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                      FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
                                                                                                                                                                                                                                                                                                                                                                    FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS
                                                                                                                                                                                                      1 MOMSPALTCLVIJGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
                                                                                                                                                                                                                                          GVASVLAMLQLITGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
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                                                                                                                                                                                     1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; DB 8;
4.4e-190;
                                                                                                                                 100.0%; Score 2071;
100.0%; Pred. No. 4.4
ive 0; Mismatches
erythema multiforme, contact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ39257 standard; protein;
                                                                                                                                                             Conservative
                                                                                                                                               Best Local Similarity
Matches 402; Conser
                                                                                                        Seguence 402 AA;
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleotide sequences given in farction in the individual and altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in the specification and which is between about 16 and 1000 nucleotides in specification and which is between about 16 and 1000 nucleotides in the contraint of a comprising the contraint of a comprising the contraint of a comprising an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and contraint comprising the contraint and variant infarction. The novel detection method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction. This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: Thi sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                   an individual who has an altered risk for developing infarction by detecting a single nucleotide polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK
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100.0%; Pred. No. 4.4e-190;
ive 0; Mismatches 0;
                                                                                                                           Claim 10; SEQ ID NO 920; 145pp;
                                                                                         the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
WPI; 2004-533949/51.
N-PSDB; ADQ38429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                      Identifying
myocardial i
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RESULT 20

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Human myocardial infarction-associated gene derived protein, SEQ ID 919.
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                                                                   Myocardial infarction; detection; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                      Claim 10; SEQ ID NO 919; 145pp; English
                                                                                                                                                                                                                 Iakoubova 0;
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        ADQ39256 standard; protein; 402
                                                                             cardiant; gene therapy; human
                                                                                                                                                         20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466112P.
23-SEP-2003; 2003US-0504955P.
                                                                                                                                           22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                 Cargill M, Devlin JJ,
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N-PSDB; ADQ38428.
                                                                                                            #02004058052-A2.
                                                                                             sapiens
                                      18-NOV-2004
                       ADQ39256;
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ADQ39256
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide bolymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an or altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least cut especification in the specification and solated polypeptide acid sequences given in the specification; an isolated polypeptide acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an intended sequence given in the specification; an antibody comprising the manifest of specification and which is between about 16 and 1000 nucleotides in the specification; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting an snP given in the polypeptide; and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an snP polymucleotide; a buffer and an enzyme; method detecting an snP polymucleotide; and an enzyme; method for identifying an agent useful in treating or preventing composition for treating or preventing myocardial infarction. The novel detection method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction. The sequence represents the protein of a human myocardial infarction. This sequence was not shown in the specification. The sequence has come from a electronic sequence listing downloaded from the MIPO website. Sequence 402 AA;

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1 MQMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY 60
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                                      0; Indels
     100.0%; Score 2071; DB 8; 100.0%; Pred. No. 4.4e-190;
                                    0; Mismatches
                                    402; Conservative
Query Match
Best Local Similarity
                      Best Loca
Matches
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Length 402;

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180
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                                                                                                                                                                         FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV 180
                                                                                                                                                           CHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
                                                                                                                                                                                                      FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating a mammal having a tumor of glial origin comprising cells that express a type A or B glial tumor antigen by contacting the cells with a composition comprising first and second binding agents.
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                                                                                                                              DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLPHKSDGSTVSVPMMAQTNKFNYTEFTTPD
                                           GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
                                                                                                                                                                                                                                                           STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
                                                                                                                                                                                                                                                STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
                                                                                                                                                                                                                                                                                                                                                                                      lumor-associated antigenic target polypeptide TAT458.
                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; diagnosis; therapy; tumor;
tumor-associated antigenic target polypeptide; TAT.
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                                                                                                                                                                                                                                                                                                                       ADV70216 standard; protein; 402
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
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N-PSDB; ADV70121.
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                                                                                                                                                                                                                                                                                                                                                                                             PSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360
mammal. The method is useful in treating a mammal having a tumor of glial origin comprising cells that express a type A or B glial tumor antigen. This sequence represents a human tumor-associated antigenic target polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New catalytic nucleic acid that specifically cleaves an mRNA encoding
                                                                                                                                                                                                                   GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
                                                                                                                                                                                                                                                            301 FSLETEVDLRKPLENIGMTDMFRQFQADFTSLSDQBPLHVAQALQKVKIEVNESGTVASS
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                                                                                                                                                                                                                                              FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
                                                                                                                                                                                                                                                                                              DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD
                                                                                                                                                1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
                                                                                                                         Gaps
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                                                                                                 Length 402;
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                                                                                                                        Indels
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                                                                                                  100.0%; Score 2071; DB 9;
100.0%; Pred. No. 4.4e-190;
ive 0; Mismatches 0;
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23-APR-2003; 2003WO-US012767.
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                                                                                                                           Matches 402; Conservative
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                                                                                                                Similarity
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                                                                             Sequence 402
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The invention relates to a catalytic nucleic acid that specifically cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1).

Cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1).

Cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1).

Cleaves an mRNA encoding composition companition of the catalytic nucleic acid, oligonucleotide, or inhibitor of PAI-1 expression, and a carrier; (2) a method of treating a vascular disease in a subject where the catalog a vascular disease in a subject where the vascular catalogue is treated by reducing thrombin or fibrin production; (4) a method of treating a vascular disease in a subject where the vascular catalogue is treated by inhibition of PAI-1 expression; (5) a method of inhibiting thrombin and fibrin deposition in a heart or cof inhibiting smooth muscle cell proliferation in a tissue of a subject; (7) a method of inhibiting thrombin and fibrin deposition in a heart or cof inhibiting thrombin and fibrin deposition in a heart or cof inhibiting thrombin and fibrin deposition in a disease or disorder, or hemostatic disorder where the disease or disorder, or hemostatic disorder where the disease or disorder, or hemostatic disorder where the disease or disorder of a subject; (6) a method of treating a disorder of a subject; (7) a method of treating a disorder of a subject; (8) a method of treating vascular, thrombotic caid, compositions and methods are useful for treating vascular, thrombotic or hemostatic disorders. The present cardinomy crepresents human PAI-1, which is used in the exemplification of
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activator inhibitor-1 (PAI-1), useful for treating vascular,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVASVLAMLQLITGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVORDIKLVOGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
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drug screening; cancer; tumor; hyperproliferation; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
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Best Local Similarity 100.0%; Pred. No. 4.4e-190;
Matches 402; Conservative 0; Mismatches 0;
                                                      English
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        plasminogen activator inhibitor-1 (
thrombotic or hemostatic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
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                                                            Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 402 AA;
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The invention relates to identifying a mammal that will respond
therapeutically to a method of treating cancer by administering an
the special state of the process of the special appearing as AEB297650level of at least one biomarker nucleic acids appearing as AEB297650AEB29715 and/or any of the process appearing as AEB29774 given
in the specification as Table 1. The method of identifying a mammal that
will respond therapeutically to a method of identifying a mammal that
administering an epidermal growth factor receptor (EGFR) modulator cited
above further comprises measuring in the mammal the level of at least one
concerned in the level of the at least one biomarker, where a
difference in the level of the at least one biomarker, where a
difference in the level of the at least one biomarker measured in step
conceptibility or resistance to a treatment. The method is used for
cof treating cancer. Also disclosed are EGFR receptors, nucleic acids,
antibodies, microarrays and kits for determining or predicting
cusceptibility or resistance to a treatment. The method is used for
individualized genetic profiles which aid in treating diseases and
clasorders based on patient response at a molecular level, including
cancers, tumors, immunological disorders, proliferative disorders and
call signaling disorders. The present sequence is one of the EGFR
congraders based on patient sequence is one of the EGFR ö Identifying mammal that will respond therapeutically to cancer treatment by administering epidermal growth factor receptor modulator and comparing biomarker level such as lymphocyte antigen 75 or Cadherin 17, LI cadherin 61 GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120 FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV 180 FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV 180 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD 240 GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300 9 1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY 1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY immune disorder; immunomodulator; cell proliferation; cell signaling Gaps ö 100.0%; Score 2071; DB 9; Length 402; 100.0%; Pred. No. 4.4e-190; 0; Indels Jackson DG; 0; Mismatches Claim 1; SEQ ID NO 76; 264pp; English Yoganathan S, (BRIM ) BRISTOL-MYERS SQUIBB 07-JAN-2004; 2004US-0535151P. 07-JAN-2005; 2005WO-US000638 Matches 402; Conservative Ford SK, WPI; 2005-522719/53 Similarity (liver-intestine). N-PSDB; AEB29660 Sequence 402 AA; WO2005067667-A2 Homo sapiens 28-JUL-2005 Clark EA, 121 121 61 181 241 Query Match Local 유 ò a 8 g ò

360 360 FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS PSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 241 301 301 361 361 g à a ∂

Search completed: December 13, 2005, 15:50:16 Job time : 195 secs

us-10-506-406-2.rai

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TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
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Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Patent No. 5187089
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Sequence 1, Appli
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                                                                                                      December 13, 2005, 09:01:15; Search time 47 Seconds (without alignments) 707.141 Million cell updates/sec
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[1. /cgn2_6/ptodatea/1/iaa/5_COMB.pep:*
22. /cgn2_6/ptodatea/1/iaa/6_COMB.pep:*
33. /cgn2_6/ptodatea/1/iaa/H_COMB.pep:*
34. /cgn2_6/ptodatea/1/iaa/PGTUS_COMB.pep:*
35. /cgn2_6/ptodatea/1/iaa/RE_COMB.pep:*
36. /cgn2_6/ptodatea/1/iaa/Nezekfiles1.pep:*
37. /cgn2_6/ptodatea/1/iaa/Nezekfiles1.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-026-408-3
US-09-324-494A-2
US-09-902-648-3
US-10-628-395-3
US-08-121-714-6
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US-09-722-292-4
US-08-948-997-5
US-09-348-817A-5
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US-09-324-494A-3
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US-08-477-112-6
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                                                                                                                                                                                                                                                                                                        572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                        protein search, using
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Maximum DB seq length: 200000000
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Match Length DB
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Patent No. 5187089
Patent No. 5187089
Patent No. 5187089
Sequence 67, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 27, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: TX
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN RElease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,461
FILING DATE: Concurrently Herewith
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PATACT NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UMIC:006
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEFAX: (512) 418-3000
TELEFAX: (512) 414-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE: AMAIO acids
TYPE: amino acids
                                                                     US-110-037-417-67
US-110-037-417-66
US-09-722-29-3
US-09-722-29-3
US-09-722-29-3
US-09-722-29-3
US-09-948-997-3
US-08-948-997-3
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US-08-203-231-2
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US-10-628-395-2
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; Patent No. 5639726
; GENERAL INFORMATION:
          Houston
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100.0%; Score 2071; DB 1; Length 402; 100.0%; Pred. No. 4.6e-204;

single

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1488.0300002
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APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION: 202-371-2600
Query Match
Best Local Similarity 100.(
Matches 402; Conservative
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FOR SEQ ID NO:
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INFORMATION F
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Patent No. 6103498
GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSON, STEFINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSER
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COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
0; Mismatches
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NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 3080.
TELEPONE: (202) 807-1500
TELEPHONE: (202) 807-1500
TELEX: 90-4030 MRSNFOERSWSH
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
 402; Conservative
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| Patent No. 6303338
| GENERAL INPORMATION: APPLICANT: Ni et al. TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR ITLES OF INVENTION: NI HIBITOR NIMBER OF SEQUENCES: 15
| CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON AVENUE, SUITE 600 CITY: WASHINGTON AVENUE, SUITE 600 CITY: DATE OF COMMENT OF C
      Length 402;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
100.0%; Score 2071; DB 2;
100.0%; Pred. No. 4.6e-204;
ive 0; Mismatches 0;
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                                  DOLTRLVLVNALYFNGQWKTPPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD
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TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRINT APPLICATION DATA:

APPLICATION NUMBER: US/09/902,684

FILING DATE: 12-Jul-2001
                                                                                                                                                                                                                         STAVIVSARMAPEELIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
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100.0%; Pred. No. 4.6e-204;
ive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION UNBER: 09/026,408
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,688
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MOLECTLE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-902-684-3
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.
Matches 402; Conservative
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APPLICANT: LAWRENCE, Daniel A
APPLICANT: STERNASSON, Steingrimur P
APPLICANT: STERNASSON, Steingrimur P
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES
FILE REFERENCE: 30523/167
CURRENT APPLICATION NUMBER: US/09/324,494A
CURRENT FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
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4.6e-204;
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100.0%; Pred. No. 4.6e-204
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0; Mismatches
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Best Local Similarity 100.0%;
Matches 402; Conservative 0;
             402 amino acids
                                                                                                                                     Best Local Similarity 100.
Matches 402; Conservative
                        TYPE: amino acid
STANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-026-408-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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             ENGTH:
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Best Local S
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GTREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/121,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE:
CLASSIFICATION NOMBER: 05/05/121//14
PILING DATE:
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 00530/072001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                Query Match
Best Local Similarity 100.
Matches 402; Conservative
US-10-628-395-3
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                 GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
                                    61 GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
                                                                                                          DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD 240
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                                                                                                                                                                                                                                      GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
STATE: DC
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-1934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/026,408
FILING DATE: 19-FEB-2001
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0300002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/628,395
FILING DATE: 29-011-2003
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10628395
Patent No. 6893870
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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61 GVASVLAMLQLTTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
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      Length 402;
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; Sequence 6, Application US/08121714
; Patent No. 5470970
; Patent No. 5470970
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
100.0%; Score 2071; DB 2;
100.0%; Pred. No. 4.6e-204;
ive 0; Mismatches 0;
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GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
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Sequence 6, Application US/08477112

Patent No. 2905023

GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: NASPIN, A NOVEL SERPIN WITH
TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       96.9%; Score 2007; DB 1;
99.7%; Pred. No. 1.6e-197;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAVIVSARMAPEELIMDRPFLFVVRHNPT 390
       FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fracer, Jania K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 06570/002002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 0110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fish & Richardson P.C.
07/938,823
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                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.7
Matches 389; Conservative
                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        amino acid
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STREET: 22
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US-08-477-108A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300
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                                                                                                                                                                                                                                                                                                         61 GVASVLAMLQL/TIGGETQQQIQAAMGFKIDDKGMAPALRHL/YKELMGPWNKDEISTTDAI 120
                                                                                                                                                                                                                                                                                                                                FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS 360
                                                                                                                                                                                                                                                          FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSBVERARFIINDWVKTHTKGMISNLLGKGAV
                                                                                                                                                                                                                                        1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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                                                                                                                                                                         Length 390;
                                                                                                                                                                                                        Indels
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Patent No. 5801001
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
APPLICANT: Zou, Zhiqiang
APPLICANT: Anisowizz, Anthony
TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
                                                                                                                                                                       96.9%; Score 2007; DB 1; 99.7%; Pred. No. 1.6e-197; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
STATE:
STATE:
COUNTRY:
U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE:
MEDIUM TYPE:
COMPUTER:
SOFTWARE:
MOSTRAFFING SYSTEM:
MS-DOS (Version 5.0)
SOFTWARE:
MOSTRAFFICE (Version 5.1)
CURRENT APPLICATION DATE:
TLING DATE:
JUNG 7, 1995
TLING DATE:
JUNG 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAVIVSARMAPEEIIMDRPFLFVVRHNPT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11
CORRESSONDERGE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93
       (617) 542-8906
                                                                                                                                                                                          Best Local Similarity 99.7
Matches 389; Conservative
               TELEX: 200154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 390
                                                                                      TYPE: amino acid STRANDEDNESS:
                                                                                                                       TOPOLOGY:
US-08-121-714-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-477-108A-6
       TELEFAX:
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RESULT 11
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; Sequence 6, Application PC/TUS9308322
; GENERAL INFORMATION:
APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD 240
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llarity 99.7%; Pred. No. 1.6e-197;
Conservative 1; Mismatches 0;
COMPUTER: IBM PS/2 Model 502 or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordberfect (Version 5.1) CURRENT APPLICATION DATA: WS/08/477,112 FILING DATE: CLASSIFICATION DATA: US/08/477,112 CLASSIFICATION DATA: WS/08/477,112 FILING DATE: 09/01/93 APPLICATION NUMBER: 08/121,714 APPLICATION NUMBER: 07/938,823 APPLICATION NUMBER: 07/938,823 APPLICATION NUMBER: 07/844,296 FILING DATE: 09/01/92 APPLICATION NUMBER: 07/844,296 FILING DATE: 02/28/92 APPLICATION NUMBER: 07/662,216 FILING DATE: 02/28/92 APPLICATION NUMBER: 07/662,216 FILING DATE: 02/28/91 ATMOREY APPLICATION NUMBER: 07/662,216 FILING DATE: 02/28/91 ATMOREY APPLICATION NUMBER: 07/662,216 FILING DATE: 02/28/91 ATMOREY ATMORET ATMOREMATION:
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REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 065
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: (617) ...
TELERAX: 200154
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-477-112-6
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Best Local Similarity
Matches 389; Conserv
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                                                                                   SITAE: MASSACHISECTS
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPETECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08322
FILING DATE: 02/04/92
FILING DATE: 02/04/92
APPLICATION WUMBER: 07/938,823
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/944,296
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/662,216
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
APPLICATION NUMBER: 34,819
RECISTRATION NUMBER: 00530/072001
TELECOMMUNICATION NUMBER: 00530/072001
TELECOMMUNICATION NUMBER: 00530/072001
TELEPHONE: (673) 5.4.0000
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Fish & Richardson
                  225 Franklin Street
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Matches 389; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                        Massachusetts
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ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
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US-08-948-997-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 379;
Sequence 3, Application US/08840204
Patent No. 6103498
GENERAL INFORMATION:
APPLICANT: LAVENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUN P.
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MORRISON & FOERSER
STREET: 2000 PENNSYLVANIA AVENUE, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                           STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1958; DB 2; I Pred. No. 1.7e-192;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY FAGENT INFORMATION:
ATTORNEY FAGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30,807
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEFAX: (202) 822-0168
TELEFAX: 90-4030 MESNFORENSWSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 animo acids
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Best Local Similarity 100.
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                               STREET: 2000 PEN
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-840-204-3
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Sequence 3, Application US/09324494A

Sequence 3, Application US/09324494A

Patent No. 6489143

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
TITLE OF INVENTION NUMBER: US/09/324,494A

CURRENT FILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 379

TYPE: PRT

ORGANISM: Homo sapiens
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APPLICANT: HASTINGS, GREGG
APPLICANT: COLEMAN, TIM
APPLICANT: COLEMAN, TIM
APPLICANT: LAWRENCE, DANIEL
TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF
TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.5%; Score 1958; DB 2; Sest Local Similarity 100.0%; Pred. No. 1.7e-192; Matches 379; Conservative 0; Mismatches 0;
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LENGTH: 402
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          LENGTH: 402
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Sequence 4, Application US/09348817A

REAL INFORMATION:

APPLICANT: Hastings et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/348,817A

CURRENT APPLICATION NUMBER: US/09/348,817A

CURRENT FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: 60/028,117

PRIOR APPLICATION NUMBER: 60/028,117

PRIOR FILING DATE: 1996-10-10

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver: 2.1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,997
FILING DATE: Oct-10-97
CLASSIFICATION: 435
ATCARSTRIATON: 435
ATCARSTRIATON: 435
REFERENCE/DOCKET NUMBER: PF336
TELECOMMUNICATION NUMBER: PF336
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAS: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERIESTICS:
LENGTH: 402 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                             linear
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Sequence 4, Application US/09722292
; Sequence 4, Application US/09722292
; Sequence 10. 654452
; Fatent No. 654452
; GENERAL INFORMATION:
; APPLICANT: Hastings et al.
; TITLE OF INVENTION: Activator
; TITLE OF INVENTION: Activator
; TITLE OF INVENTION: Activator
; TITLE OF INVENTION NUMBER: US/09/722,292
; CURRENT FILING DATE: 2000-11-28
; FRIOR APPLICATION NUMBER: 00/948,817
; FRIOR FILING DATE: 1999-07-08
; FRIOR APPLICATION NUMBER: 60/028,117
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
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86.1%; Score 1784; DB 2;
Best Local Similarity 85.3%; Pred. No. 1.4e-174;
Matches 343; Conservative 29; Mismatches 30;
                                                                                                                                                    30:
                                                                                                Query Match
Best Local Similarity 85.3%; Pred. No. 1.4e-174;
Matches 343; Conservative 29; Mismatches 30;
TYPE: PRT
CORGANISM: Bos taurus
US-09-348-817A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bos taurus
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Search completed: December 13, 2005, 09:10:56 Job time : 49 secs

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Query Match
100.0%; Score 2071; DB 3;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-902-684-3
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1626
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Sequence 920, App
Sequence 140, App
Sequence 6, Appli
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4, Appli
2, Appli
420, App
3, Appli
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Sequence 10, Appl
Sequence 6, Appli
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                                                                                                               December 13, 2005, 15:46:54; Search time 164 Seconds (without alignments) 1024.191 Million cell updates/sec
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Sequence 2,
Sequence 4,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

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3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-10-179-385-235
US-10-259-609-2
US-10-10-197-258-2
US-10-10-195-6A-420
US-10-628-395-3
US-10-741-600-919
US-10-741-600-920
US-10-852-335A-140
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US-10-506-406-2
US-10-506-46-857
US-11-060-291-8
US-11-38-995-6
US-10-558-903-3
                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    1867569 segs, 417829326 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            model
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Gapop 10.0 , Gapext 0.5
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                                                                            protein search, using
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Maximum DB seq length: 2000000000
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                                                                                OM protein
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                                                                                                                     Run on:
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Sequence 1575, Ap Sequence 5, Applisequence 5, Applisequence 5, Applisequence 5, Applisequence 5, Applisequence 297, Applisequence 185, Applisequence 185, Applisequence 186, Applisequence 136, Applisequence 186, Applisequence 88, Applisequence 88, Applisequence 67, Applisequence 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STRIE: DC
COUNTYR: USA
ZIP: 2000-3934
COMPUTER: READABLE FORM:
MEDIUM TYPE: PLOEDY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PLOEDY disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,684
FILING DATE: 12-Jul-2001
CLASSIFICATION: AUNKNOWN:
APPLICATION NUMBER: 09/026,408
FILING DATE: LUMNOWN:
APPLICATION NUMBER: US 60/024,056
FILING DATE: LUMNOWN:
APPLICATION NUMBER: US 60/024,056
ATTORNEY/AGENT INPORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 1488.0300002
TELERANCE JOUGHT INPORMATION:
TELERANCE JOUGHT INFORMATION:
TELERANCE JOU
                                                Sequence 1
Sequence 1
Sequence 1
Sequence
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; Patent No. US20020127640A1
; Patent INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INHIBITOR
                                                                                                                                                                                        US-10-631.467.1575
US-10-631.467.1595
US-10-631.467.1595
US-09-987.021-5
US-10-752-041-5
US-10-752-041-5
US-10-728-487-5
US-10-170-385-297
US-10-170-385-297
US-10-287-436A-501
US-10-287-436A-501
US-10-287-436A-1264
US-10-037-417-67
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Gaps

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Length 402; Indels

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61 GVASVLAMIQLTIGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTIDAI 120
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                   61 GVASVLAMLQLITGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTIDAI 120
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| Saquence 10, Application US/10193656
| Publication No. US20030096733A1
| GENERAL INPORMATION:
| APPLICANT: NY, Tox
| APPLICANT: NY, Tox
| APPLICANT: HI, Jinan
| TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
| FILE REFERENCE: 3810/14577-US3
| CURRENT APPLICATION NUMBER: US/10/193,656
| CURRENT FILING DATE: 2002-07-10
| PRIOR FILING DATE: 2001-07-10
| PRIOR PILING DATE: 2001-07-10
| PRIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 18
| SOFTWARE: PATENTIN VERSION 3.1
| SEC ID NO 10
                                                                                                                                  STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
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Pred. No. 3e-190;
0; Mismatches 0;
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / F05121
DATABASE ENTRY DATE: 1987-08-13
RELEVANT RESIDUES: (1). (402)
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100.0%;
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Best Local Similarity 100.0
Matches 402; Conservative
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                                                                                  61 GVASVLAMLQLTTGGETQQQ1QAAMGFK1DDKGMAPALRHLYKELMGPWNKDEISTTDA1 120
                                                                                                                                                       121 FVQRDLKLVQGFMPHFFRLPRSTVKQVDFSEVERARFIINDWVXTHTKGMISNLLGKGAV 180
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                   1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
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APPLICANT: Kalos, Michael D.

APPLICANT: Lodgs, Michael J.

APPLICANT: Lodgs, Michael J.

APPLICANT: Lodgs, Miliam T.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Jang, Yuqiu T.

APPLICANT: Jang, Yuqiu M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

FILE REFERENCE: 210121.566

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 154
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100.0%; Pred. No. 3e-190;
tive 0; Mismatches 0;
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Publication No. US20030073144A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-060-036-154
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402; Conserva
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Best Local
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APPLICANT: LAWRENCE, Daniel A
APPLICANT: LAWRENCE, Daniel A
APPLICANT: LAWRENCE, Steingrimur P
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES TH
FILE REFERENCE: 305.31/167
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/324,494A
PRIOR PILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                             GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
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100.0%; Score 2071; DB 4;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      ; Score 2071; DB 4;
; Pred. No. 3e-190;
0; Mismatches 0;
    PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER: PEGI ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 235
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Best Local Similarity 100.0
Matches 402; Conservative
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US-10-170-385-235
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US-10-259-609-2
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US-10-259-609-2
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                                                                                                              Sequence 6, Application US/10128706
Publication No. US20030199463A1
GENERAL INFORMATION:
APPLICAMY: ITESCU, SILVIU
TITLE OF INVENTION: A DAS ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
FILE REFERENCE: 0575/66601
CURRENT APPLICATION NUMBER: US/10/128,706
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 6.
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Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0
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APPLICANT: Kan, On
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
TITLE OF INVENTION: ANALYSIS METHOD
CURRENT APPLICATION NUMBER: US/10/170,385
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APPLICANT: Mundy, Christopher Robe:
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katle Mary
APPLICANT: Raymer, William Nigel
APPLICANT: Rayner, William Nigel
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CRGANISM: HOMO SAPIENS
US-10-128-706-6
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US-10-170-385-235
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APPLICANT: GORLATOVA, NATALIA
APPLICANT: GORLATOVA, NATALIA
APPLICANT: CRANDALL, DAVID L.
TITLE OF INVENTION: MUTANT PROTEINASE-INHIBITORS AND USES THEREOF
FILE REPERENCE: 030523-0187
CURRENT PAPLICATION NUMBER: US/10/197,258
CURRENT FILING DATE: 2002-07-18
NUMBER OF SEQ ID NOS: 12
SSCTWARE: PATENTIN Ver. 2.1
SSGT ID NO 2
LENGTH: 402
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Publication No. US20040053233A1
GENERAL INFORMATION:
APPLICANT: Lorens, James B.
APPLICANT: AL, Weiduan
APPLICANT: Holland, Sacha
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-004100US
                                                                                                                                                                                                              ; Sequence 2, Application US/10197258; Publication No. US20040014190A1; GENERAL INFORMATION:
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US-10-197-258-2
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US-10-231-956A-420
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US-10-197-258-2
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Publication vo. US20030217371A1
GENERAL INFORMATION:
APPLICANT: Vaughan, Douglas E.
APPLICANT: Eren, Mesut
APPLICANT: Declerk, Paul J.
TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON TITLE OF INVENTION:
TITLE OF INVENTION: ANIMAL
TITLE OF INVENTION ANIMAL
CURRENT APPLICATION NUMBER: US/10/368,995
CURRENT APPLICATION NUMBER: US/10/368,995
CURRENT PILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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0; Mismatches 0;
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Best Local Similarity 100.
Matches 402; Conservative
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ORGANISM: Human
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US-10-368-995-4
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US-10-368-995-4
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100.0%; Score 2071; DB 5; Length 402; 100.0%; Pred. No. 3e-190;
         ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.0300002

TELEPHONE: 202-371-2500

TELEPHONE: 202-371-250

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHAPACTERISTICS:

LENGTH: 402 amino acid

TYPE: amino acid

STRANDEDNESS: single
TOPOLCGY: linear

MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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100.0%; Score 2071; DB 4
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0
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CORGANISM: Homo sapiens
US-10-741-600-919
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Best Local Similarity
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US-10-741-600-919
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CORRESPONDENCE ADDRESS:
ADDRESSEE STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC. Compatible
COMPUTER: IBM PC. Compatible
OPERATING SYSTEM: PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Publication No. US20040086978A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINGEN ACTIVATOR
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                                                                                                                                                                                  Length 402;
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100.0%; Pred. No. 3e-190;
iive 0; Mismatches 0;
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APPLICATION NUMBER: US/10/628,395
FILING DATE: 29-Uul-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: 19-FEB-2001
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
CURRENT APPLICATION NUMBER: US/10/231,956A CURRENT FILING DATE: 2001-08-30 NUMBER OF SEQ ID NOS: 522 SSCTVARLE: PSELSEQ for Windows Version 3.0 SEQ ID NO 420 LENGTH: 402
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Matches 402; Conservative
                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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US-10-231-956A-420
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US-10-628-395-3
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Sequence 919, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION: US20050026169A1
GENERAL INFORMATION: GENERAL MICHAEL OF INVENTION: MICHAEL OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLO01499
CURRENT FILING DATE: 2003-12-22
CURRENT FILING DATE: 2003-12-22
CURRENT FILE OF UNION WHOMEN: VS-12997
SOFTWARE: FASTESQ for Windows Version 4.0
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Length 402;
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Sequence 6, Application US/10512496;
Publication No. US20050148527A1;
GENERAL INFORMATION:
A PAPLICANT: ITESCU, SILVIU
ITILE OF INVENTION:
FILE REFERENCE: 0575/66601-A-PCT-US
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                                                                                                                                                                                     Sequence 140, Application US/10852335A

Sequence 140, Application US/10852335A

Sequence 140, Application US/10852335A

Sequence 140, Application US/10852335A

GENERAL INFORMATION: PHILLIPS

TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumors of Glial Origin

FILE REFERENCE: P5103R-US

CURRENT PELING DATE: 2004-05-24

PRIOR APPLICATION NUMBER: US 60/548,299

PRIOR APPLICATION NUMBER: US 60/473,238

PRIOR APPLICATION NUMBER: US 60/473,238

NUMBER OF SEQ ID NOS: 190

SEQ ID NO 140

LENGTH. 400
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Best Local Similarity
Matches 402; Conserv
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ORGANISM: Homo
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US-10-512-496-6
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Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARCILL,
TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FagtSEQ for Windows Version 4.0
SEQ ID NO 920
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100.0%; Pred. No. 3e-190;
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; ORGANISM: Homo sapiens
US-10-741-600-920
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Sequence 2, Application US/10506406

Sequence 3, Application No. US20050158295A1

GENERAL INFORMATION:

APPLICANT: Swiezrc, Rafal

APPLICANT: Selman, Jercy

APPLICANT: Jankun, Jercy

APPLICANT: Jankun, Jercy

APPLICANT: Jankun, Jercy

APPLICANT: Skrzypczak-Jankun, Ewa

TITLE OF INVENTION: MODIFIED PLASMINGEN ACTIVATOR INHIBITOR

TITLE OF INVENTION: TYPE-1 AND METHODS BASED THEREON

FILE REPERBUCE: 9471-011-99

CURRENT APPLICATION NUMBER: US/10/506,406

CURRENT PILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-03-04

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                           Length 402;
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                                                                                                                                        Query Match 100.0%; Score 2071; DB 5; Best Local Similarity 100.0%; Pred. No. 3e-190; Matches 402; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/512,496
CURRENT FILING DATE: 2004-10-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VERSION 3.1
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ORGANISM: Homo sapiens
                                                                                      TYPE: PRT
ORGANISM: HOMO SAPIENS
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LENGTH: 402
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Length 402;

DB 5;

100.0%; Score 2071;

Query Match

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Publication No. US20050208496A1

FUBLICATION NO. US20050208496A1

GENERAL INFORMATION:
APPLICANT Genox Research Inc.
TITLE OF INVENTION: Method for testing for broncheal asthma, or c.
TITLE OF INVENTION: disease
FILE REPERENCE: 3462.1005-000

CURRENT APPLICATION NUMBER: US/10/631,467

CURRENT FILING DATE: 2003-07-31

PRIOR PLICATION NUMBER: JP 2003-07712

PRIOR PLICATION NUMBER: JP 2002-229312

PRIOR PLICATION NUMBER: JC 2003-03-00

PRIOR FILING DATE: 2002-08-06

NUMBER OF SEQ ID NOS: 2086

SOFTWARE: PARCHIN VERSION 3.1

SEQ ID NOS: 2086
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100.0%; Score 2071; DB 5;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0;
Best Local Similarity 100.0%; Pred. No. 3e-190; Matches 402; Conservative 0; Mismatches 0;
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US-10-631-467-857
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APPLICANT: Bren, Meaut
APPLICANT: Bren, Meaut
APPLICANT: Bren, Meaut
APPLICANT: Declerk, Paul J.
TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
TITLE OF INVENTION: ANIMAL
FILE REFERENCE: 1242/43
CURRENT APPLICATION NUMBER: US/10/368,995
CURRENT FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
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Publication No. US20030216321A1

GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: LAWERENCE, Daniel A

APPLICANT: STEFANSSON, Steingrimur P

TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR TYPE 1 (PAI-1) AND USES THIS
FILE REFERENCE: 30523/167

CURRENT APPLICATION NUMBER: US/10/259,609

CURRENT APPLICATION NUMBER: US/09/324,494A

PRIOR APPLICATION NUMBER: US/09/324,494A

PRIOR PILING DATE: 1999-06-02

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PATENTING ON SECOND 3.1

EMBIT OF SECOND NOS: 29

SOFTWARE: PATENTING DATE: 1379

TYPE: PRIOR PILING DATE: 1379
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100.0%; Pred. No. 9e-183
ive 0; Mismatches
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                   APPLICANT: Vaughan, Douglas E.
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US-10-259-609-3
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Best Local Similarity
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Best Local Similarity
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ORGANISM: Human
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US-10-259-609-3
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                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/11060291
; Sequence 8, Application US/050186608A1
; PUBLication No. US20050186608A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Byron
; TITLE OF INVENTION: Treatment of Obesity and Diabetes
; TITLE OF INVENTION: Treatment of Obesity and Diabetes
; FILE REFERENCE: GTC-223
; CURRENT APPLICATION NUMBER: US/11/060,291
; CURRENT APPLICATION NUMBER: 60/545,790
PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; SEQ ID NO 8
; LENGTH: 402
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US-10-368-995-6
Sequence 6, Application US/10368995
; Publication No. US20030217371A1
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ORGANISM: Homo sapiens
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                                                                              YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR 323
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Patent No. US20020143165A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc. et al.

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen

TITLE OF INVENTION: Activator

FILE REFRENCE: PF336P1

CURRENT APPLICATION NUMBER: US/09/957,485

CURRENT FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: US 09/521,664

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOLIRLVLVNALYFNGOWKIPFPDSSIHRRLFHKSDGSIVSVPMMAQINKFNYTEFITPD
241 YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLBNLGMTDMFR
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85.3%; Pred. No. 1.2e-162;
ive 29; Mismatches 30;
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Best Local Similarity 85.3%
Matches 343; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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ORGANISM: Bos taurus
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US-09-957-485-4
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                                                                        84 AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST 143
                                                                                                                      VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP 203
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llarity 100.0%; Pred. No. 2e-179;
Conservative 0; Mismatches 0; Indels
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       0; Mismatches
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         379; Conservative
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Matches 379; Conserv
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Publication No. US20030217371A1

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APPLICANT: Vaughan, Douglas E.
APPLICANT: Vaughan, Douglas E.
APPLICANT: Eren, Mesut
APPLICANT: Declark, Danie
TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
TITLE OF INVENTION: ANIMAL
TITLE OF INVENTION: 16
SURFARMY APPLICATION NUMBER: US/10/368,995
CURRENT FILING DATE: 2003-02-19
NUMBER OF SEQ ID NOS: 16
SOFTWARES PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GRYYDILELPYHGNTLSMLJAAPYEKEVPLSALTSILDAELISQWKGNMTRLTRLLVLPK 300
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85.3%; Pred. No. 1.2e-162;
iive 29; Mismatches 30;
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le : 172 secs
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Matches 343; Conserv
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ORGANISM: Cow
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APPLICANT: Yepes et al.

TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator
FILE REFERENCE: PF3362
CURRENT APPLICATION NUMBER: US/09/987,021
CURRENT APPLICATION NUMBER: 09/957,485
PRIOR APPLICATION NUMBER: 09/957,485
PRIOR APPLICATION NUMBER: 09/722,292
PRIOR APPLICATION NUMBER: 09/722,292
PRIOR APPLICATION NUMBER: 09/521,664
PRIOR FILING DATE: 2000-11.14
PRIOR FILING DATE: 2000-11.14
PRIOR FILING DATE: 1099-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-10-10
PRIOR FILING DATE: 1999-10-10
PRIOR FILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
TRACTH: AD2
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85.3%; Pred. No. 1.2e-162;
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US-10-368-995-2
; Sequence 2, Application US/10368995
                                                                Sequence 4, Application US/09987021
Patent No. US20020165147A1
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Best Local Similarity 85.3
Matches 343; Conservative
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                                             US-09-987-021-4
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Sequence 1581, Ap Sequence 1488, Ap Sequence 185, App Sequence 20, Appli Sequence 112, Appli Sequence 112, Appli Sequence 1498, Ap Sequence 1498, Ap Sequence 131, Appli Sequence 131, Appli Sequence 131, App Sequence 131, App Sequence 131, App Sequence 131, App Sequence 131, Appli Sequence 131, Appli Sequence 131, Appli Sequence 131, Appli Sequence 130, Appli Appli Sequence 130, Appli A
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Sequence 2, Appli
Sequence 3126, Appli
Sequence 3126, Appli
Sequence 100, Appl
Sequence 1121, Appli
Sequence 1728, Appli
Sequence 1728, Appli
Sequence 1728, Appli
Sequence 1557, Appli
                                                                                                                                                         December 13, 2005, 09:13:06; Search time 12 Seconds (without alignments) 187.078 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpāa/US00_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpāa/US07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpāa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpāa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US17_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-11-86-284-188

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US-10-621-234-900

US-10-623-155-110

US-11-05-276-2

US-11-10-623-155-112

US-11-10-623-155-112

US-11-10-131-826A-498

US-10-131-826A-498

US-10-131-826A-498

US-10-131-821-234-185

US-11-07-15-245A-2

US-11-07-15-245A-2

US-10-131-826A-130

US-11-057-058-54
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
Match Length DB
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33, 31, 1067	Sequence 52, Appli Sequence 6, Appli Sequence 6, Appli Sequence 8, Appli Sequence 5, Appli	80, 47, 362	254, 14, A 1066,	Sequence 1102, App Sequence 64, Appl Sequence 4, Appli Sequence 1120, Ap
US-11-057-058-33 US-11-057-058-31 US-11-108-172-1067	US-11-065-943-52 US-11-091-643-6 US-10-525-710-6 US-10-336-263A-8	US-11-0/3-103 US-10-131-826A-80 US-11-089-551A-47 US-11-074-176-362	US-11-074-176-254 US-11-058-727-14 US-11-108-389-14 US-10-793-626-1066	US-11-108-172-1102 US-11-057-058-64 US-11-058-727-4 US-11-108-389-4 US-10-821-234-1120
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## ALIGNMENTS

SULT 1 -10-821-234-1581 cacquence 1581, Application US/10821234 publication No. US20050255114A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Labar, Ivan APPLICANT: Labar, Ivan APPLICANT: Andarmani, Susan APPLICANT: Tang, Y. Tom APPLICANT: Tang, Y. Tom TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia FILE REPERENCE: 821A CURRENT APPLICATION NUMBER: US/10/821,234 CURRENT APPLICATION NUMBER: US/60/462,047 PRIOR FILING DATE: 2003-04-07 NUMBER OF SEQ ID NOS: 1704 SOFTWARE: pt. SEQ_genes Version 1.0 SEQ ID NO 1581 IENGTH: 402 IENGTH: 402 TYPE: PRT ORGANISM: Homo sapiens	ch 100.0%; Score 2071; DB 6; Length 402; 11 Similarity 100.0%; Pred. No. 7.3e-179; 402; Conservative 0; Mismatches 0; Indels 0; Gaps	1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY	1 GVASVLAMLQLTTGGETQQQQQQAAMGFKIDDKGMAPALRHLYKELMGPWNKDBISTTDAI 	1 PVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV	1 DOLTRLVLVNALYFNGOWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPD	1 GHYYDILELPYHGDTLSWFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 	1 FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS
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APPLICANT: Thibodeau, Stephen N.
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APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION: TITLE OF INVENTION: METHODS FOR IDENTIFICATION NUMBER: US/10/301,822
PRIOR PELICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 185
LENGTH: 398
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APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andermani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERENCE: 821A
CURRENT PAPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 36.7%; Score 761; DB 7; Length 39 Best Local Similarity 41.3%; Pred. No. 3.5e-61; Matches 157; Conservative 77; Mismatches 142; Indels
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                                  Monahan, John E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo Sapiens
US-11-186-284-185
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                                                                                                                                                                                                                                               Sequence 1488, Application US/10821234
| Publication No. US2005025114A1
| GENERAL INFORMATION:
| APPLICANT: Labat, Ivan
| APPLICANT: Stache-Crain, Birgit
| APPLICANT: Tang, Y: Tom
| TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
| TILLE OF INVENTION: UNMBER: US 60/462,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| PRIOR APPLICATION NUMBER: US 60/462,047
| PRIOR SEQ ID NOS: 1704
| SOFTWARE: Dt SEQ Genes Version 1.0
324 QFQADFTSL-SDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFL 382 :|:| :: | |||: || || |||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 MGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTV 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 TESSTPLSAIIPHISTKTIDS#MSIMVPKRVQVILPKFTAVAQTDLKEPLKVLGITDMFD 318
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41.3%; Pred. No. 3.5e-61;
ive 77; Mismatches 142; Indels
                                                                              402
                                                                                                         361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
                                                                            STAVIVSARMAPEEI IMDRPFLFVVRHNPTGTVLFMGQVMEP
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVVRHNPTGTVLFMGQVMEP 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1488
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Length 398;

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APPLICANT: Hu, walke, Boris
APPLICANT: Walke, D. Wade
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: Novel Human Protease Inhibitor and Polynucleotides Encoding the S
FILE REFERENCE: LEX-0283-USA
CURRENT APPLICATION NUMBER: US/11/096,276
CURRENT PILING DATE: 2005-03-31
PRIOR FILING DATE: 2003-04-17
PRIOR PRILING DATE: 2003-04-17
PRIOR PRILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR PRILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 MMTQKGLYRIGFIEEVKAQILEMRYTKGKLSMFVLLPSHSKDNLKGLEELERKITYEKMV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLFRSTVKQVDF-SEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNG 196
                                                                                                                          QWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTL 256
                                                                                                                                                          QWDREFKKENTKEEKFWMNKSTSKSVQMMTQSHSFS---FTFLEDLQAKILGIPYKNNDL 242
                                                                                                                                                                                                SMFIAAPYEKEVPLSALTNILSAQLISHW--KGNMTRLPRLLVLPKFSLETEVDLRKPLE 314
                                                                                                                                                                                                                                                                         315 NLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAP-- 372
                                                                                                                                                                                                                                                                                                302 AMGMGDAFSEHKADYSGMSSGSGLYAQKFLHSSFVAVTEEGTEAAAATGIGFTVTSAPGH 361
15 LFQEIGKDDRHKNIFFSPLSLSAALGMVRLGARSDSAHQIDEVLHFNBFSQNESKEPDPC
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                                                                          Length 425;
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26.2%; Pred. No. 2.6e-32;
tive 89; Mismatches 149;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/11096276; Publication No. US20050260726A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.2%
Matches 111; Conservative
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CORGANISM: homo sapiens
US-11-096-276-2
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Publication No. US20050261166A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Retter, Marc W.

APPLICANT: Facter, Marc W.

APPLICANT: Facter, Marc W.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: CANDOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REPERENCE: 210121.455C20

CURRENT APPLICATION NUMBER: US/10/623,155

CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 110

LENGTH: 391
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21.3%; Score 441; DB 6; Length 391;
Best Local Similarity 27.4%; Pred. No. 1.9e-32;
Matches 107; Conservative 92; Mismatches 165; Indels
                                                                                                                                                                        22.3%; Score 461; DB 6; Length 423; 28.8%; Pred. No. 3.4e-34; ive 76; Mismatches 162; Indels
         PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ_ID NO 900
                                                                                                                                                                                                Best Local Similarıty 20.0
Matches 119; Conservative
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US-10-623-155-110
                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                              Similarity
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                                                                                                                            ; ORGANISM: DC....
US-10-821-234-900
                                                                                    LENGTH: 423
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                       303 AWSSSENWSEESVVLSFPRFTLEDSYDLNSILQDMGITDIFDETRADLIGISPSPNLYLS 362
                                                                                            :: | :||:||:|| | |::| | ::| 363 KIIHKTFVEVDENGTQAAAATGAVVSERSLRSWVEFNANHPFLFFIRHNKTQTILFYGRV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 SRIKABEKEVVRIKAEGKEIENTEAVHQQFQKFLTEISKLTNDYELNITNRLFGEKTYLF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------AAMGFKIDD-KGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 HWKG--NMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 VQGFMPHFFRLFRSTVKQVDF-SEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GIPYKNNDLSMFVLLPNDID-GLEKIIDKISPEKLVEWTSPGHMEERKVNLHLPRFEVED 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 QALQKVKIEVNESGIVASSSTAVIVSARMAPE--EIIMDRPFLFVVRHNPTGTVLFMGQV
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                                                                                                                                                                                                                                                                        Sequence 112, Application US/10623155
Publication No. US20050261166A1
Publication No. US20050261166A1
Publication No. US20050261166A1
APPLICANT: Peckham, David W.
APPLICANT: Panger, Mary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICANTS
NUMBER OF SEQ 1D NOS: 560
SOFTWARE FEASTSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 21.2%; Score 438.5; DB 6; Length 9
Best Local Similarity 27.1%; Pred. No. 3.3e-32;
Matches 108; Conservative 91; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | : | | | : | | | | 362 FTVTSAPGHENVHCNHPFLPFIRHNESNSILFFGRESSP 400
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ORGANISM: Homo sapiens
                                                                                                                                                 400 MEP 402
                                                                                                                                                                                    423 CSP 425
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US-11-147-047-39 Sequence 39, Application US/11147047 Publication No. US2005026066881

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 FKI---DDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 DSSTHRRL-FHKSDGSTVSVPMMAQTNKFNY---TEFTTPDGHYYDILELPYHGDTLSMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 PPSYVAHLASDFGVRVFQQVAQASKDRNVVPSPYGVASVLAMLQLTTGGETQQQLQAAMG
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APPLICANT: Agarwal, Pankaj
APPLICANT: Murdock, Paul R.
APPLICANT: Murdock, Paul R.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Siang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
TITLE OF INVENTION: NOVEL COMPOUNDS
CURRENT APPLICATION NUMBER: US/11/147,047
CURRENT FILING DATE: 2005-06-07
PRIOR APPLICATION NUMBER: OF/10/221,097
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/186,916
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/186,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/186,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/186,916
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFFWARE: PARESEQ FOR WINDOWS VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-11-071-580-1
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REPRENCE: P3330R10128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/05931
PRIOR APPLICATION NUMBER: 60/05931
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR PRIOR PRIOR DATE: 1997-09-19
PRIOR PRIOR APPLICATION NUMBER: 60/05958B
PRIOR FILING DATE: 1997-09-19
PRIOR PRIOR APPLICATION NUMBER: 60/05958B
PRIOR PRIOR APPLICATION NUMBER: 60/05958B
PRIOR PRIOR PRIOR DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.0%; Score 394.5; DB 6; Length 444; 28.4%; Pred. No. 3.4e-28; tive 81; Mismatches 174; Indels 15;
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                       Watanabe, Colin K
Wood, William
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Best Local Similarity 28.4%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-498
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US-10-821-234-1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 EVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQ 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.2%; Score 398.5; DB 7; Length 444; 28.6%; Pred. No. 1.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
APPLICANT: AND ALL AND ALL AND ALL APPLICANT: LU, Dyung Alna M. TITLE OP INTERNION: PROTEASES AND PROTEASE INHIBITORS FILE REFERENCE: PP-0727 PCT CURRENT APPLICATION NUMBER: US/11/071,580 CURRENT FILING DATE: 1999-08-09 PRIOR APPLICATION NUMBER: 60/147,986 PRIOR APPLICATION NUMBER: 60/147,986 PRIOR APPLICATION NUMBER: 60/147,986 PRIOR PILING DATE: 1999-10-21 PRIOR FILING DATE: 1999-10-21 SOFTWARE: PERL PROGRAMME: PERL P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 088718CD1
US-11-071-580-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 RHNPTGTVLFMGQVMEP 402
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 28.6%
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-131-826A-498
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APPLICATION NUMBER: US/10/301,822
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APPLICANT: Berger, Allianna Fracy L. APPLICANT: Guillemette, Tracy L. APPLICANT: Guillemette, Tracy L. APPLICANT: Schlegel, Robert APPLICANT: Schlegel, Robert APPLICANT: Monahan, John E. APPLICANT: Monahan, John E. APPLICANT: Thibodeau, Stephen N. APPLICANT: Thibodeau, Stephen N. APPLICANT: Thibodeau, Stephen N. TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: THERAPY OF COLON CANCER FILE REFERENCE: MPM01-029PZNM CURRENT APPLICATION NUMBER: US/11/186,284

CURRENT APPLICATION NUMBER: US/11/186,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 QLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 QGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 DTFV-NASRILYSSSPRVLSNNSDANLELINTWVAKNINNKISRLLDSLPSD--TRLVLL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 NALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYD---- 245
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                                                                                                                APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPERBNES: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PLESQ Genes Version 1.0
SEQ ID NO 1458
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Sequence 1458, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
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107; Conservative
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US-10-821-234-1458
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US-11-186-284-187
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Best Local S
Matches 107
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Sequence 1331, Application US/10821234
; Sequence 1311, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
    APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tang, Y. Tom
; TILLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 82.A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO S: 1704
; SEQ ID NO 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 --DAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : : : | | | : | : | | | : | 248 ---DEKEKLOIVEMPLAHKLSSLIILMPHHVE-PLERLEKLLTKEQLKIWMGKMQKKAVA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 KD--VERTDGALLVNAMFFKPHWDEKFHHKMVDNRGFMVTRSYTVGVMMHRTGLYNYYD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 FTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRL 295
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PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 187
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Sequence 18, Application US/11010874

Sequence 18, Application US/11010874

Sequence 18, Application US/11010874

Sequence 18, Application No. US20050250694A1

GENERAL INFORMATION:

APPLICATON: M. Jian.Xian

TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND

TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND

TITLE OF INVENTION: COMPOUNDS USFUL IN MAKING AND USING SAME

FILE OF INVENTION: PIBROSIS AND METHODS OF MAKING AND USING SAME

FILE OF INVENTION NUMBER: US/11/010,874

CURRENT FILING DATE: 2004-10-12

PRIOR FILING DATE: 2003-10-10

PRIOR PELING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: 60/520,647

PRIOR PELING DATE: 2003-12-11

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 18

LENGTH: 362
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                                                                                           307 VDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIV 366
                                                                                                                      323 GEVTKSLQEMKLQSLFD--SPDFSKITG-KPIKLTQVEHRAGFEWNEDGAGTTFSPGLQP 379
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247 LELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETE 306
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                                            264 AQLPLTG-SMSIIFFLPLKVTQNLTLIEESLTSEFIHDIDRELKTVQAVLTVPKLKLSYE
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Job time : 14 Becs
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US-11-010-874-18
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; Sequence 2, Application US/11077716
; Publication No. US2050260180A1
; GENERAL INFORMATION:
APPLICANT: WEI, LISA
APPLICANT: RASMUSSEN, HENRIK S
TITLE OF INVENTION: MATERIALS AND METHODS FOR TREATING VASCULAR LEAKAGE IN THE EYE
FILE REFRENCE: 233988
CURRENT PAPLICATION NUMBER: US/11/077,716
CURRENT PAPLICATION NUMBER: US 60/552,768
PRIOR FILING DATE: 2004-03-12
PRIOR FILING DATE: 2004-03-12
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 MPHFFRLFRSTVK-----QVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRL 186
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                                                                                   15 ALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTG 74
                                                                                                              15 ALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTG
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                                       56;
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                 23.7%; Pred. No. 3.4e-20;
iive 87; Mismatches 189; Indels
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                                         94; Conservative
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                   Best Local Similarity
Matches 94; Conserv
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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using sw model protein search, OM protein December 13, 2005, 09:01:30 ; Search time 39 Seconds Run on:

(without alignments) 991.773 Million cell updates/sec

Title:

US-10-506-406-2 2071 1 MOMSPALTCLVLGLALVFGE......FVVRHNPTGTVLFMGQVMEP 402 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 of hits satisfying chosen parameters: Total number

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* Database :

pirl:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description					plasminogen activa		proteinase inhibit	glia-derived nexin	neuroserpin precur	serpin - pig	kallikrein-bindin	leukocyte elastase	alpha-1-antiprotei	contrapsin-related	alpha-1-antiprote	leupin precursor	alpha-1-antitrypsi	alpha-1-antiprotei	elastase inhibitor	serine proteinase	alpha-1 proteinase	antithrombin III	alpha-1 proteinase	antithrombin III	plasminogen activa	intracellular coa	placental thrombin	alpha-1 proteinase	111111111111111111111111111111111111111
	Ω	ITHUP1	806745	JC4265	A35032	A34761	148717	B27496	A37274	S70647	<b>S38962</b>	B29131	A42421	JX0267	823675	JX0154	138202	ITRT	S54981	S27383	808102	149473	XHHU3	149472	159611	A32853	A55533	A48681	149470	
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*	Match	100.0	86.1	84.3	81.1	78.5	38.5	38.2	36.7	29.9	24.3	24.1	24.0	r	23.5	23.5	23.3	23.2	23.2			23.0		22.8	22.7	22.6		22.6		•
	8	2071	1784	1746	1680	1626	796.5	791.5	761	620	503.5	498.5	498	490	487.5	486	483.5	480	480	479	479	476	474.5	472	470.5	469	468.5	468	468	
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aquamons cell carc	plasminogen activa	serine proteinase	alpha-1-antichymot	contrapsin precure	antithrombin III -	alpha-1-antitrypsi	probable proteinas	MAP1 protein - myx	alpha-1 proteinase	plasminogen activa	hypothetical prote	alpha-1-antitrypsi	antithrombin III p	thyroxine-binding	serine proteinase
138201	S19896	831507	JH0494	JX0129	JX0364	A54968	A24470	B36418	149474	S20047	AH1903	S21097	\$28219	A39567	S11320
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390	416	418	418	418	431	413	361	369	413	415	374	416	465	418	408
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## ALIGNMENTS

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plasminogen activator inhibitor 1 precursor [validated] - human
NiAlternate names: plasminogen activator inhibitor, endothelial
C;Species: Homo sapiens (man)
C;Species: J1-Mar-1988 #sequence revision 31-Mar-1988 #text\_change 05-Oct-2004
C;Accession: A28107; S02551; A26996; I59126; J30397; A25693; A256146; A25996; A25
R;Bosma, P. J.; van den Berg, E. A.; Kooistra, T.; Siemieniak, D.R.; Slightom, J.L.
J; Biol. Chem. 263, 9129-9141, 1988
A;Title: Human plasminogen activator inhibitor-1 gene. Promoter and structural gene nucl
A;Reference number: A28107
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-402 cBOS>
A;Cross-references: UNIPROT: P05121; UNIPARC: UP10000000CAB; GB:J03764; NID:g189564; PIDN:
R;Strandberg, L.; Lawrence, D.; Ny, T.
Eur. J. Blochem. 176, 609-616, 1988
A;Title: The organization of the human-plasminogen-activator-inhibitor-1 gene. Implication
A;Reference number: S02551; MUID:89005111; PMID:3262512
A;Accession: S02551;

A; Molecule type: DNA A; Residues: 1.14, T', 16-402 <STR> A; Residues: 1.14, T', 16-402 <STR> A; Cross references: UNIPARC: UDIO0001731AA; EMBL: X13338; NID: G35244; PIDN: CAA31722.1; PID A; Note: the complete translation is not annotated in GenBank entries HSPAI11, HSPAI12, H R; Loskutoff, D.J.; Linders, M.; Keijer, J.; Veerman, H.; van Heerikhuizen, H.; Pannekoek Biochemistry 26, 3763-3768, 1987 A; Title: Structure of the human plasminogen activator inhibitor 1 gene: nonrandom distra A; Reference number: A26996; MUID: 88000586; PMID: 2820474

A, Accession: A26996

A; Molecule type: DNA
A; Residues: 1-402 < LOS.
A; Residues: 1-402 < LOS.
A; Residues: 1-402 < LOS.
A; Cross-references: UNIPARC: UPI0000000CAB; GB:M22321; GB:M17121; NID:g189576; PIDN:AAA60
A; Cross-references: UNIPARC: UPI0000000CAB; GB:M22321; GB:M17121; NID:g189578) has the cod
A; Note: the sequence in GenBank entry HUMPAIB2, release 109.0, (PID:g189578) has the cod
R; van Zonneveld, A.J.; Curriden, S.A.; Loskutoff, D.J.
A; van Zonneveld, A.J.; Curriden, S.A.; Loskutoff, D.J.
A; ricle: Type 1 plasminogen activator inhibitor gene: functional analysis and glucocorti
A; Reference number: IS9126; MUID:88289754; PMID:2840665

A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,COSS-references: UNIPARC:UPI00000038D; GB:J03836; NID:g189579; PIDN:AAA60010.1; PID
R;Follo, M.; Ginsburg, D.
R;Follo, M.; Ginsburg, D.
A,Title: Structure and expression of the human gene encoding plasminogen activator inhib
A,Reference number: JS0397; MUID:90128289; PMID:2612914

A;Molecule type: DNA A;Residues: 85-86;88-93;166-171;231-236;298-302;331-336;360-365;388-393 <POL> A;Cross-references: UNIPARC:UP1000011EC8E; UNIPARC:UP100001731AB; UNIPARC:UP100001731AC 1B1; GB:M33136; NID:9189543 A;Note: sequences of the intron/exon boundaries are shown

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A;Molecule type: mRNA
A;Residues: 153-235 <PEP>
A;Cross-references: UNIPARC:UP1000016C357; EMBL:X52906; NID:9598; PIDN:CAA37094.1; PID:95
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J. Call Biol. 111, 743-755, 1990
A;Title: Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induc A;Reference number: A35855; MUID:90338128; PMID:1696269
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Eur. J. Biochem. 176, 81-87, 1988
A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and heat
oma cells. Vascular endothelial cells may be the primary site of synthesis of plasma C; Comment: Glycosylation is not required for inhibitory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GVASVLAMLOLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAI 120
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                                                                                                                                                             A;Cross-references: GDB:120297; OMIM:173360
A;Rap position: 7q21.3-7q22
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1; 363/1; 391/1
C;Superfamily: serpin
C;Superfamily: serpin
C;Keywords: glycoprotein; serine proteinase inhibitor
F;1-23/Domain: signal sequence #status predicted <857G>
F;24-402/Product: plasminogen activator inhibitor-1 #status predicted F;23-2388.352/Bainding site: carbohydrate (Asn) (covalent) #status predicted F;369/Inhibitory site: Arg (plasminogen activator) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasminogen activator inhibitor-1 precursor - bovine
NyAlternate names: endothelial-cell plasminogen activator inhibitor; PAI-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Feb-1990 #sequence revision 22-Apr-1995 #text_change 05-Oct-2004
C;Accession: S06745; A35855; S01324; S10906
R;Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
Nucleic Acids Res. 17, 8872, 1989
A;Title: cDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).
A;Reference number: S06745; MUID:90067867; PMID:2587231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 2071; DB 1; Best Local Similarity 100.0%; Pred. No. 2.5e-155; Matches 402; Conservative 0; Mismatches 0;
                                                                                                                                   A; Gene: GDB: PAII; PLANH1
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A; Residues: 1-402 <MIM>
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A; Residues: 17-402 kWINA
A; Residues: 17-402 kWINA
A; Cross-references: UNIPARC: UPI000016AE5E; GB: X04744; NID: 935275; PIDN: CAA28444.1; PID: 9
A; Note: part of this sequence, including the amino end of the mature protein, was confir
B; Ny, T.; Sawdey, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.
Broc. Natl. Acad. Sci. U.S.A. 83, 6776-6780, 1986
A; Title: Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-
A; Reference number: A25895; MUID: 86313660; PMID: 3092219
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A;Residues: 1-14,'T',16-47 <AND1>
A;Cross-references: UNIPARC:UPI000016AESC; GB:X04729; NID:g35263; PIDN:CAA28438.1; PID:g
A;Accession: B25651
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A;Residues: 370-375 <STO>
A;Cross-references: UNIPARC:UPI00001731B5
C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:UKHUT
fibrinolysis. High concentrations of this protein have been associated with human throm
C;Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339).
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A; Residues: 20-402 < NYTS
A; Residues: 20-402 < NYTS
A; Residues: 20-402 < NYTS
B; Andreasen, P.A.; Riccio, A.; Welinder, K.G.; Douglas, R.; Sartorio, R.; Nielsen, L.S.; PEBS Lett. 209, 213-218, 1986
A; Title: Plasminogen activator inhibitor type-1: reactive center and amino-terminal hete A; Reference number: A91371; MUID:87080762; PMID:3025016
                                                                                                                                                                          A;Accession: A25693
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kosedues: 1-402 <PAN>
A;Cosedues: 1-402 <PAN>
A;Cosedues: 1-202 <PAN: A;Cosedues: 1, Dan
A;Title: CDNA cloning of human plasminogen activator-inhibitor from endothelial cells: A;Reference number: A92766; MUID:87058123; PMID:3097076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli of a plasminogen activator inhibitor (PA
PMID:3026837
    R;Pannekoek, H.; Veerman, H.; Lambers, H.; Diergaarde, P.; Verweij, C.L.; van Zonneveld, BMBO J. 5, 2539-2544, 1986
BMBO J. 5, 2539-2544, 1986
A;Title: Endothelial plasminogen activator inhibitor (PAI): a new member of the serpin gasterence number: A;Reference numbe
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A;Residues: 1-402 <GIN>
A;Cross-references: UNIPARC:UPI000000CAB; GB:MI6006; NID:g189541; PIDN:AAA60003.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Wun, T.C.; Kretzmer, K.K.
FEBS Lett. 210, 11-16, 1987
A;Title: CDNA cloning and expression in E.
A;Reference number: A29100; MUID:87105925;
A;Accession: A29100
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site: Arg (plasminogen activator) #status predicted
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A; Residues: 1-402 <ZEH>
                                                        Query Match
Best Local Similarity
Matches 343; Conserv
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        F;367/Inhibitory
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C;Species: Mustela vison (American mink)
C;Date: 19-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C;Date: 19-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C;Date: 19-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C;Date: 10-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C;Date: 10-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 05-Oct-2004
C;Chang, T.H.; Hamilton, R.T.; Nilsen-Hamilton, M.
Gene 162, 303-306, 1995
A;Thle: Cloring of the mink plasminogen activator inhibitor type-1 messenger RNA: An mF
A;Reference number: JC4265, MUID:96032362; PMID:7557448
A;Residues: 1-400 <CHU>
A;Residues: 1-400 <CHU>
A;Residues: 1-400 <CHU>
A;Residues: 1-400 <CHU
A;Cross-references: UNIPROT:P50449; UNIPARC:UPT000131217; EMBL:X58541; NID:91164923; PI
A;Residues: 1-400 <CHU
A;Residu
                                      A, Accession: S01324
A, Molecule type: protein
A, Molecule type: Double type
A, Cromment: Three types of PAI have been identified. PAI-1 is an acid-stable glycoprotein
C, Comment: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, an
ysis.
C, Comment: Glycosylation is not a prerequisite for inhibitory activity.
C, Superfamily: serpin
C, Keywords: glycoprotein; serine proteinase inhibitor
C, Keywords: glycoprotein; serine proteinase inhibitor
F, 1-23/Domain: signal sequence #status predicted < SIG>F, 23-2, 288, 352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F, 322, 288, 352/Binding site: carbohydrate (Asn) (covalent) #status predicted
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86.1%; Score 1784; DB 1; Length 402;

Best Local Similarity 85.3%; Pred. No. 9.8e-133;

Matches 343; Conservative 29; Mismatches 30; Indels
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                 PMID:3262060
              A; Reference number: S01324; MUID: 88329072;
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A;Cross-references: UNIPARC:UP10000131219; GB:M24067; NID:g577500; PIDN:AAA56856.1; PID A;Cross-references: UNIPARC:UP1000131219; GB:M-A.; Pepinsky, R.B.; Keski-Oja, J. R;Newman, M.J.; Lane, E.A.; Iannotti, A.M.; Nugent, M.A.; Pepinsky, R.B.; Keski-Oja, J. Endocrinology 126, 2336-2246, 1990 A;Title: Characterization and purification of a secreted plasminogen activator inhibitor on in transformed NRK cells.
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A; Residues: 24-48 KNEW.
A; Residues: 24-48 KNEW.
A; Cross-references: UNIPARC:UPI00001731B6
B; Cross-references: UNIPARC:UPI00001731B6
B; Olson Jr., Jr.; Shiverick, K.T.; Ogilvie, S.; Buhi, W.C.; Raizada, M.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991
A; Title: Angiotensin II induces secretion of plasminogen activator inhibitor 1 and a tix-Arcession: A39120
A; Accession: A39120
A; Status: preliminary
A; Molecule type: protein
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A; Residues: 1-402 < ARLO.
A; Residues: 1-402 < CARLO.
A; Residues: 1-402 < CARLO.
A; Cross-references: UNIPROT: P20961; UNIPARC: UPI0000131219; GB:J05206; NID:g205965; PIDN
R; Zeheb, R.; Gelehrter, T.D.
R; Zeheb, R.; Gelehrter, T.D.
A; S99-468, 1988
A; Title: Cloning and sequencing of cDNA for the rat plasminogen activator inhibitor-1.
A; Reference number: JT0490; MUID:89211983; PMID:3149611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasminogen activator inhibitor 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 Haequence revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A35032; JT0490; A6051; A3912, A3120
R;Bruzdainski, C.J.; Riordan-Johnson, M.; Nordby, E.C.; Suter, S.M.; Gelehrter, T.D.
J. Biol. Chem. 265, 2078-2085, 1990
A;Title: Isolation and characterization of the rat plasminogen activator inhibitor-1
A;Reference number: A35032; MUID:90130456; PMID:2298740
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                                                                                                                                                                                                                                                                                                                                                                                                                           239 GRYYDILELPYHGDILSMFIAAPYEKDVPLSALTNILDAQLISQWKGNMTRRLKLLVLPK
                                                                                                                                                                       GVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDBISTTDAI
                                                                                                                                                                                                                                                                                               DQLTRLVLVNALYFNGQWKTPPPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTBFTTPD
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                                                                                                                        1 MOMSPALTCLVLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPY
                                                                  Gape
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A;Accession: A60581
84.3%; Score 1746; DB 2;
llarity 85.3%; Pred. No. 9.6e-130;
Conservative 25; Mismatches 32;
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9

360

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proteinase inhibitor nexin I precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148717; 870772; 835731
R;Vassalli, J.D.; Huarte, J.; Bosco, D.; Sappino, A.P.; Sappino, N.; Velardi, A.; Wohlwen
BRBO J. 12, 1871-1879, 1993
A;Title: Protease-nexin I as an androgen-dependent secretory product of the murine seminals, A;Reference number: 148717; MUID:93259128; PMID:8491179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-86 <VAS>
A; Residues: 1-86 <VAS>
A; Cross-references: UNIPARC:UP1000016CFC8; EMBL:X70946; NID:g57930; PIDN:CAA50285.1; E
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993
C; Genetics: A; Genetics: C; Superfamily: serpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q07235; UNIPARC:UPI000004078; EMBL:X70296; NID:g551064; A;Accession: S70772
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                           GLEYDVVELPYQRDTLSMFIAAPFEKDVHLSALTNILDAELIRQWKGNMTRLPRLLILPK 300
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                                                                                                   FSLETEVDLRKPLENIGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASS
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                                                                                                                                                                        FVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAV
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-397/Product: proteinase inhibitor nexin I #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.5%; Score 796.5; DB 2;
43.0%; Pred. No. 5.5e-55;
tive 74; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: 148717
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-397 <RES>
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Matches 159; Conservative
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A34761
plasminogen activator inhibitor 1 homolog mrl - mouse
c;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A44761; S48208
R;Prendergast, G.C.; Diamond, L.E.; Dahl, D.; Cole, M.D.
R;Prendergast, G.C.; Diamond, L.E.; Dahl, D.; Cole, M.D.
A;Title: The C-myc-regulated gene mrl encodes plasminogen activator inhibitor 1.
A;Reference number: A44761; MUID:90158593; PMID:2406566
A;Accession: A44761
A;Molecule type: mRNA
A;Residues: 1-402 - RPRS
A;Cross-references: UNIPROT:P22777; UNIPARC:UPI00000298B9; GB:M33960; NID:g200219; PIDN: R;Lijne: Characterization of the murine plasma fibrinolytic system.
A;Recence number: 848202; MUID:95010076; PMID:7523120
A;Accession: S48208
A;Molecule type: protein
A;Recession: S48208
A;Molecule type: protein
A;Residues: 'W', 24-29 - &LIJ>
A;Residues: 'W', 24-29 - &LIJ>
A;Residues: Ww., 24-29 - &LIJ>
A;Residues: Will serpin
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                                                                                                                                                                                                                                                                                                                   Gaps
A;Residues: 24-43,'G' <OLS>
A;Cross-references: UNIPARC:UP100001731B7
C;Genetics:
A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1; 363/1; 391/1
C;Superfamily: serpin
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-402/Product: plasminogen activator inhibitor-1 #status experimental
F;88,232,288,352/Binding site: carbohydrate (Asn) (covalent) #status pred
F;369/Inhibitory site: Arg (plasminogen activator) #status pred
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                 81.1%; Score 1680; DB 1; Length 402; 80.8%; Pred. No. 1.5e-124; ive 36; Mismatches 41; Indels
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316; Conserva
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Best Local Similarity
Matches 325; Conserv
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Nighternate names: glia-derived neurite promoting factor; proteinase inhibitor 7; protein Nighternate names: glia-derived neurite promoting factor; proteinase inhibitor 7; protein Nighternate names: glia-derived neurite promoting factor; proteinase glia-derived nexin I precursor, splice form alpha C; pate: 31-Dec-1991 #med-1991 #med-1
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A; Molecule type: mRNA
A; Residues: 1-238, R', 331-398 <SOM>
A; Residues: 1-238, R', 331-398 <SOM>
A; Cross-references: UNIPPRC: UPI00000D9F3; GB:M17783; NID:g183063; PIDN:AAA35883.1; PID
R; Gloor, S.; Odink, K.; Guenther, J.; Nick, H.; Monard, D.
R; Gloor, S.; Odink, K.; Guenther, J.; Nick, H.; Monard, D.
A; Gloor, S.; Aja-derived neurite promoting factor with protease inhibitory activity belon
A; Reference number: A26061; MUID:87051740; PMID:2877744
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A;Title: Protease nexin. Properties and a modified purification procedure.
A;Reference number: A24051; MUID:85207723; PMID:3997857
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                                                                            94 MAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFWPHFFRLFRSTVKQVDFSEVE 153
                                                                                                                                   213 HKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 LINILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMPRQFQADFTSL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 IIPHISIKTINSMMNTMVPKRMQLVLPKFTALAQTDLKEPLKALGITEMFEPSKANFAKI 327
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                                                                                                                                                                                                                                        154 RARFIINDWVXTHTKGMISNLLGKGAVDQ-LTRLVLVNALYFNGQWKTPFPDSSTHRRLF
                                                                                                                                                                                                                                                                                           148 SACDAINFWVKNETRGMIDNLLSPNLIDSALTKLVLVNAVYFKGLWKSRFQPENTKKRTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 VAGDGKSYQVPMLAQLSVPRSGSTKTPNGLWYNPIELPYHGESISMLIALPTESSTPLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 SDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGT
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A; Residues: 1-398 <MCG1>
A; Cross-references: UNIPROT: P07093; UNIPARC: UPI0000049599
A; Experimental source: splice form beta
A; Accession: JJ0010
A; Molecule type: mRNA 311-398 <MCG2>
A; Cross-references: UNIPARC: UPI00000009F3
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A,Residues: 1-259,'S',261-398 <GLO>
A,Cross-references: UNIPARC:UP1000017631D
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A;Residues: 20-47 <SCO>
A;Cross-references: UNIPARC:UPI000017631E
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388 ILFLGQVNKP 397
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                                                                                                                                                                                      333 SDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGT 392
                                                                                                                                                                                                                                                                                                                                                  208 VAGDGKSYQVPMLAQLSVFRSGSTRTPNGLWYNPIELPYHGESISMLIALPTESSTPLSA 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 VLFMGQVMEP 402
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ILFLGQVNKP 397
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A;Cross_references: UNIPARC:UP100001762F0
A;Note: the sequence from Fig. 6 is inconsistent with that from Fig. 5 in having 256-Asn
C;Superfamily: serpin
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                                                                                                                                                                                                                   PKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSST-AVIVSARMAPEE-IIMDRP 380
                                                                                                                                                                                                                                                                                                              174 ALTHLVLINALYPKGNWKSQFRPENTRIFSFIKDDETEVQIPMMYQQGEFYYGEFSDGSN 233
                                                                                                                                                                                                                                                                                                                                                                           PDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVL 298
                                                                                                                                                                                                                                                                                                                                                                                                                         234 EAGGIYQVLEIPYEGDEISMMIVLS-RQEVPLVTLEPLVKASLINEWANSVKKQKVEVYL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 -ERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGOWKTPFPDSSTHRRL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 FHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYD----ILELPYHGDTLSMFIAAPYEKE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRINKKDSKTVKMMYOKKKF-----PFGYIKELKCRVLELPYOGKDLSMVILLPDSIE 237
                                                                                                 LITGGETQQQIQAAMGFKIDDKGMAPALRH----LYKBLMGPWNKDE----ISTTDAIF 121
                                                                                                                                            LGAHGTTLKEIRHSLGF-----DSLKNGEEFTFLKDLSDMATTEESHYVLNMANSLY 113
                                                                                                                                                                                         VQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVD 181
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                                   LISITALINIPSKAFKTINFPDETIAELS----VNVYNQLRAAREDENILFCPLSIAIAMGMIE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change 05-Oct-2004
         VLGLALVFGEGSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 FGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGF-KIDDKGMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 ALRHLYKELMGPWNKDEIS----TTDAIFVQRDLKLVQGFWPHFFRLFRSTVKQVDFSEV
                                                                                                                                                                                                                                                                                   OLTRLVLVNALYFNGOWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEF---TT
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R;Teschauer, W.F.; Mentele, R.; Sommerhoff, C.P.
Bur. J. Blochem. 217, 519-526, 1993
A;Title: Primary structure of a porcine leukocyte serpin. A;Reference number: $38962; MUID:94039085; PMID:7901009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.3%; Score 503.5; DB 2; Best Local Similarity 33.2%; Pred. No. 6.1e-32; Matches 127; Conservative 70; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serpin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
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A,Status: preliminary
A,Molecule type: protein
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C;Species: Gallus gallus (chicken)
C;Species: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C;Accession: 370647; 877695
R;Osterwalder, T.; Contartese, J.; Stoeckli, E.T.; Kuhn, T.B.; Sonderegger, P.
EMBO J. 15, 2944-2953, 1996
A;Title: Neuroserpin, an axonally secreted serine protease inhibitor.
A;Reference number: $70647; MUID:96272154; PMID:8670795
A;Altile: Nouroserpin, an axonally secreted serine protease inhibitor.
A;Reference number: $70647; MUID:96272154; PMID:8670795
A;Residues: 1-410 <-OSTI>
A;Residues: 1-410 <-OSTI>
A;Residues: 1-410 <-OSTI>
A;Residues: 1-409:243-257;288-293;309-317 <-OST2>
A;Coss-references: UNIPARC:UPI000017632B; UNIPARC:UPI000017632C; UNIPARC:UPI000017632D;
C;Superfamily: serpin
C;Superfamily: serpin
C;Keywords: serrine proteinase inhibitor
F;1-16/Domain: signal sequence #status predicted <-SIG>
F;17-410/Product: neuroserpin #status experimental <-MAT>
C;Genetics:
A;Gene: GDB:PI7; PNI
A;Crose-references: GDB:378380; OMIM:177010
A;Map position: 2q33-2q35
C;Superfamily: serpin
C;Kaywords: alternative splicing; glycoprotein; serine proteinase inhibitor
C;Kaywords: alternative splicing; predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-398/Product: glia-derived nexin I, splice form beta #status experimental <MATA>
F;20-398/Product: glia-derived nexin I, splice form beta #status predicted
F;118,159,384/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;365/Inhibitory site: Arg (thrombin, urokinase) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 MGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVD-QLTRLVLVNALYFNGQWKTPFP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 DSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFQADFTSL-SDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFL 382
                                                                                                                                                                                                                                                                                                                                                                                                        21 HFNPLSLEELGSNTGIQVFNQIVKSRPHDNIVISPHGIASVLGMLQLGADGRTKKQLAMV 80
                                                                                                                                                                                                                                                                                                                                                                           HHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAA
                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                      Length 398;
                                                                                                                                                                                                                                                                                   36.7%; Score 761; DB 2; Length 39 41.3%; Pred. No. 3.5e-52; ive 77; Mismatches 142; Indels
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FFIRHNPTGAVLFMGQINKP 398
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Best Local Similarity 41.33
Matches 157; Conservative
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Matches 136; Conserva
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A;Molecule type: protein
M. Measidues: 1-41, "E', 43-325, 'VD', 326-379 < DUB2>
A;Residues: 1-41, "E', 43-325, 'VD', 326-379 < DUB2>
A;Cross-references: UNIPARC:UDI00001762E9
R;Kordula, T.; Dubin, A.; Schooltink, H.; Koj, A.; Heinrich, P.C.; Rose-John, S.
R;Kordula, T.; Dubin, A.; Schooltink, H.; Koj, A.; Heinrich, P.C.; Rose-John, S.
A;Kordula, T.; Dubin, A.; Schooltink, H.; Koj, A.; Heinrich, P.C.; Rose-John, A.
A;Title: Molecular cloning and expression of an intracellular serpin: an elastase inhib!
A;Reference number: S34062; MUID:93319507; PMID:7687128
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N;Alternate names: plasminogen activator inhibitor-2 homolog
N;Alternate names: plasminogen activator inhibitor-2 homolog
C;Species: Equie caballus (domestic horse)
C;Species: Bquue caballus (domestic horse)
C;Accession: A42421; A37276; S34062
C;Accession: A42421; A37276; S34062
C;Accession: A542421; A37276; S34062
B;Dubin, A.; Travis, J.; Enghild, J.J.; Potempa, J.
A;Dubin, Chem. 267, 6576-6583, 1992
A;Title: Equine leukocyte elastase inhibitor. Primary structure and identification as a A;Reference number: A42421; MUID:92202200; PMID:1551869
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A;Residues: 1.379 cDUB1>
A;Cross-references: UNIPROT:PO5619; UNIPARC:UPI000012D513; PIDN:AAB21885.1; PID:g247842
A;Experimental source: leukocyte
A;Residues: 1-69,'C',71-72,'A',74-193,'D',195-249,'V',251-384,'V',386-416 <OHK>
A;Cross-references: UNIPARC:UPI00001762F5
C;Genetics:
A;Introna: 11/1; 302/3; 352/3
A;Introna: 11/1; 302/2; 352/3
C;Superfamily: serpin
C;Keywords: glycoprotein; serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GKWKVPFNPNDTFESEFYLDEKRSVKVPMM-----KIKDLTTPYIRDEELSCSVLELKY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.1%; Score 498.5; DB 2; 30.2%; Pred. No. 1.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Mismatches 154;
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A,Molecule type: mRNA
A,Residues: 1-379 <KOR>
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Best Local Similarity
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A; Recreates number: S11319; NULD: 90300039; FAULT: 97719
A; Redidues: 11-97, VV, 99-112, H', 113-386, P', 388-416 cPAG>
A; Redidues: 11-97, VV, 99-112, H', 113-386, P', 388-416 cPAG>
A; Redidues: 11-97, VV, 99-112, H', 113-386, P', 388-416 cPAG>
A; Redidues: 11-97, VV, 99-112, H', 113-386, V'; Le Gm. G.; Mariller, M.; Szpirer, J.; Szpirer, R; Pages, G.; Rouayrenc, J. F.; Rossi, V.; Le Gm. G.; Mariller, M.; Szpirer, J.; Szpirer, J.; Rossi, 1900
A; Reference number: JN0106; MUID: 91078650; PMID: 2258058
A; Residues: J1-97, VV, 99-325, P', 327-416 cPAZ>
A; Residues: J1-97, VV, 99-3416 cCHA>
A; Residues: J1-97, VV, 99-416 cCHA>
A; Residues: Residues: J1-97, VV, 99-416 cCHA>
A; Residues: Residues: J1-97, VV, 99-416 cCHA>
A; Residues: Residues: J1-97, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rallikrain-binding protein precursor - rat
Nallikrain-binding protein ilke protease inhibitor; growth hormone-induced proteinase
C; Species: Ratuus norvegicus (Norway rat)
C; Species: Ratuus norvegicus (Norway rat)
C; Species: Ratuus norvegicus (Norway rat)
C; Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text change 05-Oct-2004
C; Accession: B29131; A29448; S11319; JN0106; A40810; A3789; JX0156; S08099; S08101
R; Yoon, J.B.; Towle, H.C.; Seelig, S
J. Biol. Chem. 262, 4284-4289, 1987
A; Title: Growth hormone induces two mRNA species of the serine protease inhibitor gene f
A; Reference number: A92632; MUID:87166046; PMID:3494016
A; Residues: 1.416 < YOO>
A; Rosidues: 1.416 < YOO
A; Ros
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A; Molecule type: mRNA
A; Residues: 1-97, V' 99-416 < LEC>
A; Cross-references: UNIPARC: UPI00001282B0
R; Pages, G.; Rouayrenc, J.F.; le Cam, G.; Mariller, M.; le Cam, A.
R; Pages, G.; Rouayrenc, J. F.; le Cam, G.; Mariller, M.; le Cam, A.
A; Title: Molecular Characterization of three rat liver serine-protease inhibitors affect
A; Reference number: S11318; MUID: 90306038; PMID: 1694763
                                                            GS-RADLTGMSEARDLFISKVVHKSFVEVNEEGTEAAAATXGIAVFAMLMPEEDFIADHP 356
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FIFFIRHNPSSNILFLGRLSSP 378
                                                                                                                                                                                                 FLFVVRHNPTGTVLFMGQVMEP 402
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A;Cross-references: UNIPROT:Q03734; UNIPARC:UPI0000029D55; EMBL:X55148; NID:g50443; PIDN A;Experimental source: strain BALB/c A;Experimental source: strain BALB/c Bringlis, J.D.; Lee, M.; Hill, R.E. Submitted to the EMBL Data Library, December 1992 A;Reference number: S31505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 145-312, 'R', 314-418 < ING>
A, Cross-treferences: UNIPARC: UDI00000E7F9A, EMBL: X69832, NID: 954174; PIDN: CAA49486.1, PID
R, Inglis, J.D.; Hill, R.E.
EMBO J. 10, 255-261, 1991
A, Title: The murine Spi-2 proteinase inhibitor locus: a multigene family with a hypervaril
                                                                                       253 TLAS-----TVLRMDYKGNATALFL---LPDEGKLQHLEDTLTTELIAKFLAKSFRSV 303
                                                                                                                                                                                                                                                                                                304 RVRFPKLSISGTYDLKPLGKLGITQVFSD-NADLSGITEQEPLKVSQALHKAVLTIDER 362
                                                      GAVDOLTRLVLVNALYFNGOWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTN---KFNYT 234
                                                                                                                                                            235 EFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPR 294
                                                                                                                                                                                                                                                                    295 LLVLPPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNES 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contrapsin-related protein MC-7 precursor - mouse
NyAlternate names: serine proteinase inhibitor 2.4
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text_change 05-Oct-2004
C;Accession: 823675; 831506; §15632; 819078; 821870
R;Ohkubo, K.; Ogata, S.; Misumi, Y.; Takami, N.; Sinohara, H.; Ikehara, Y.
Biochem. J. 276, 337-342, 1991
A;Title: Cloning, structure and expression of cDNA for mouse contrapsin and A;Reference number: $15905; MUID:91264784; PMID:2049065
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F;1.-20/Domain: signal sequence #status predicted <SIG>
F:21-418/Product: contrapsin #status predicted <MAT>
F:104,184,269/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                           GTVASSSTAVIVSARMAPEELIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 355-418 <NN2>
A;Cross-references: UNIPARC:UP100001762F7; EMBL:X56820
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A;Residues: 355-390,'L',392-418 <IN3>
A;Cross-references: UNIPARC:UPI00001762F8; EMBL:X56820
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30.7%; Pred. No. 1.3e-30;
iive 85; Mismatches 156;
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Matches 118; Conserv
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A; Residues: 1-418 <OHK>
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     PID:
A;Cross-references: UNIPARC:UPI000012D513; GB:M91161; NID:g164240; PIDN:AAA97513.1;
C;Superfamily: serpin
C;Keywords: serine proteinase inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRLNKKDTKTVKMMYQKKKFPY-----NYIEDLKCRVLELPYQGKELSMIILLPDDI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTA-VIVSARMAPEE-IIMDR 379
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                                                                                                                                                                                                                                              7 LTCLVLGLALVFCEGSAV-----HHPPSY-VAHLASDFGVRVFQQVAQASKDRNVVFSPY 60
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                                                                                                                                                                                                                                                                                                                      97 ALRHLYKELMGPWNKDE----ISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEV
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                                                                                                           Length 379;
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                                                                                                     24.0%; Score 498; DB 2; Length 37 llarity 32.9%; Pred. No. 1.7e-31; Conservative 72; Mismatches 153; Indels
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PFIFFIRHNPSANILFLGRFSSP 379
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Best Local Similarity 30.6'
Matches 125; Conservative
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Matches 126; Conserv
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: Oryclagus
C;Accession: JX0154
R;Saito, A.; Sinohara, H.
A;Reference number: JX0154; MUD:91201273; PMID:2016265
A;Reference number: JX0154
A;Accession: JX0154
A;Ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 FROFOADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIV---SARMAPEEIIMD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFT 237
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                                                                              : | | : | | : | | : | | : | | : | | ETSEADIHQGFGHLLQRLSQPEDQDQINIGNAMFIEKDLQILAEFHEKARALYQTEAFTA 166
                                                                                                                                                                   DESEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSST 207
                                                                                                                                                                                                                                                                                                  208 HRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYD-----ILELPYHGDTLSMFIA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                262 APYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDM 321
                                  DKGMA---PALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQV 147
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                                                                                                                                                                                                         7 LTCLVLGLALVFGEGSAV----HHPPSY-VAHLASDFGVRVFQQVAQASKDRNVVFSPY
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